Fig.1

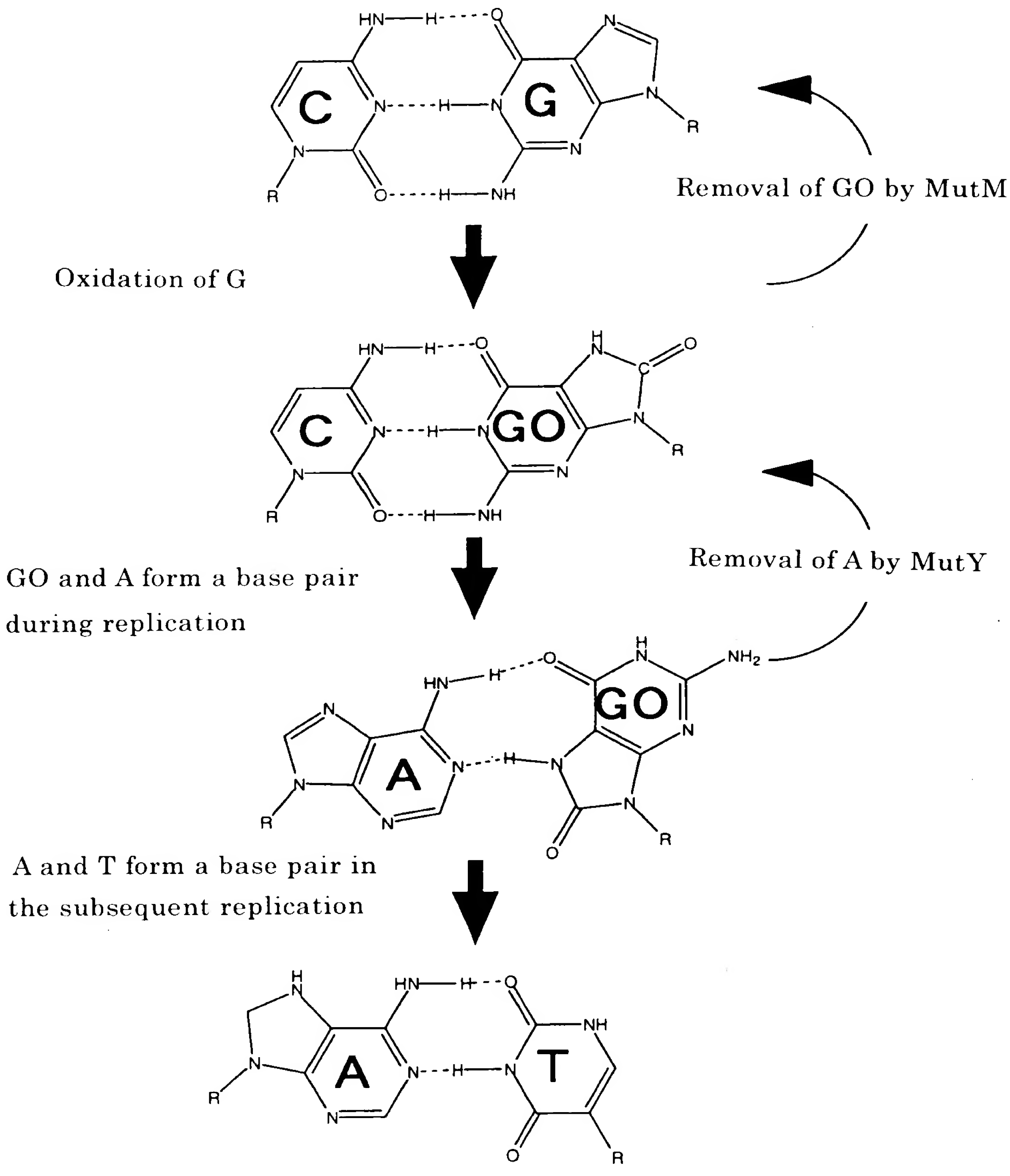

Removal of GO by MutM
Oxidation of G
Removal of A by MutY
GO and A form a base pair during replication
A and T form a base pair in the subsequent replication

Fig.2

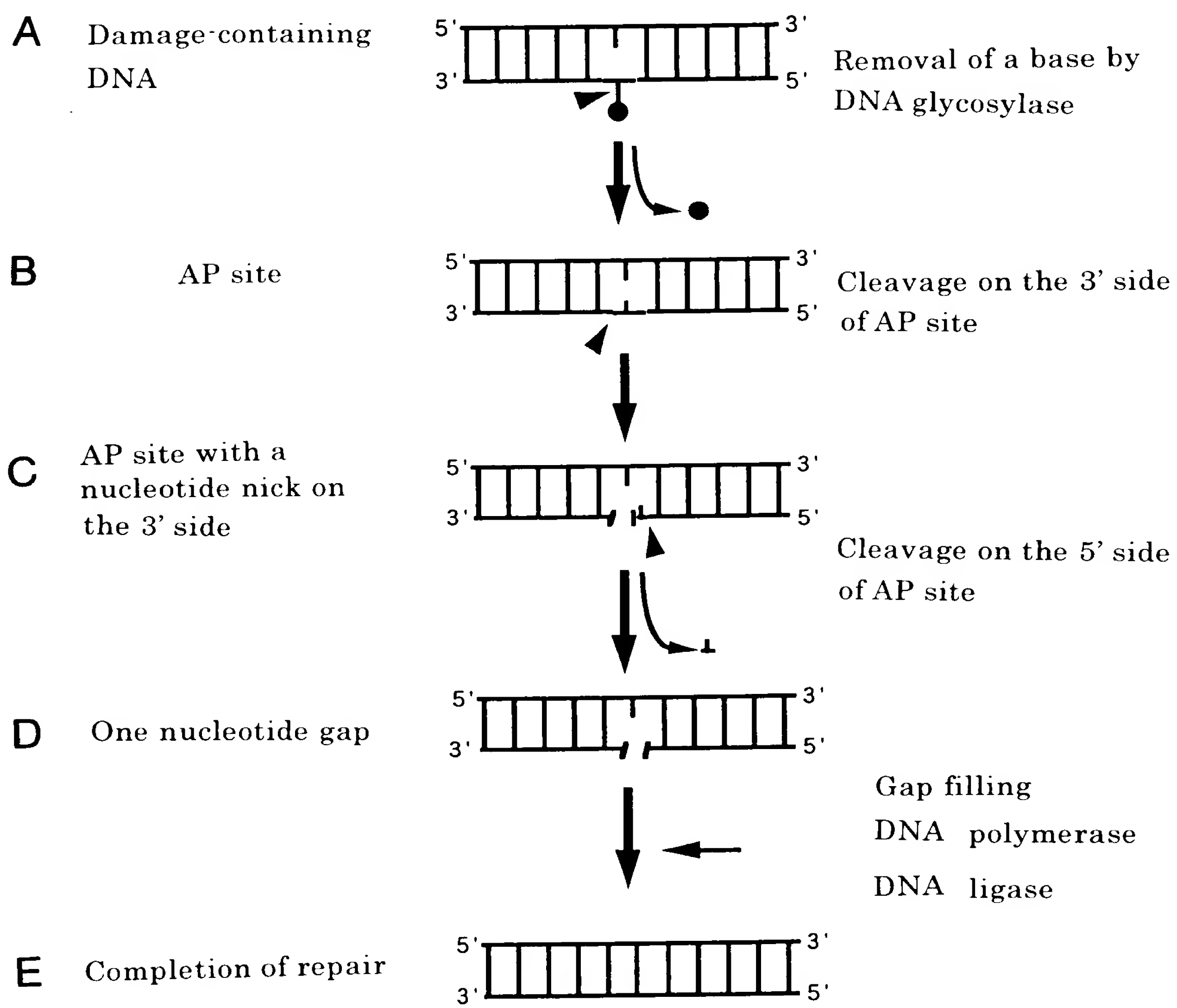

A
Damage-containing DNA
B
AP site
C
AP site with a nucleotide nick on the 3' side
D
One nucleotide gap
E
Completion of repair
5'
3'
Removal of a base by DNA glycosylase
Cleavage on the 3' side of AP site
Cleavage on the 5' side of AP site
Gap filling
DNA polymerase
DNA ligase

Fig.3

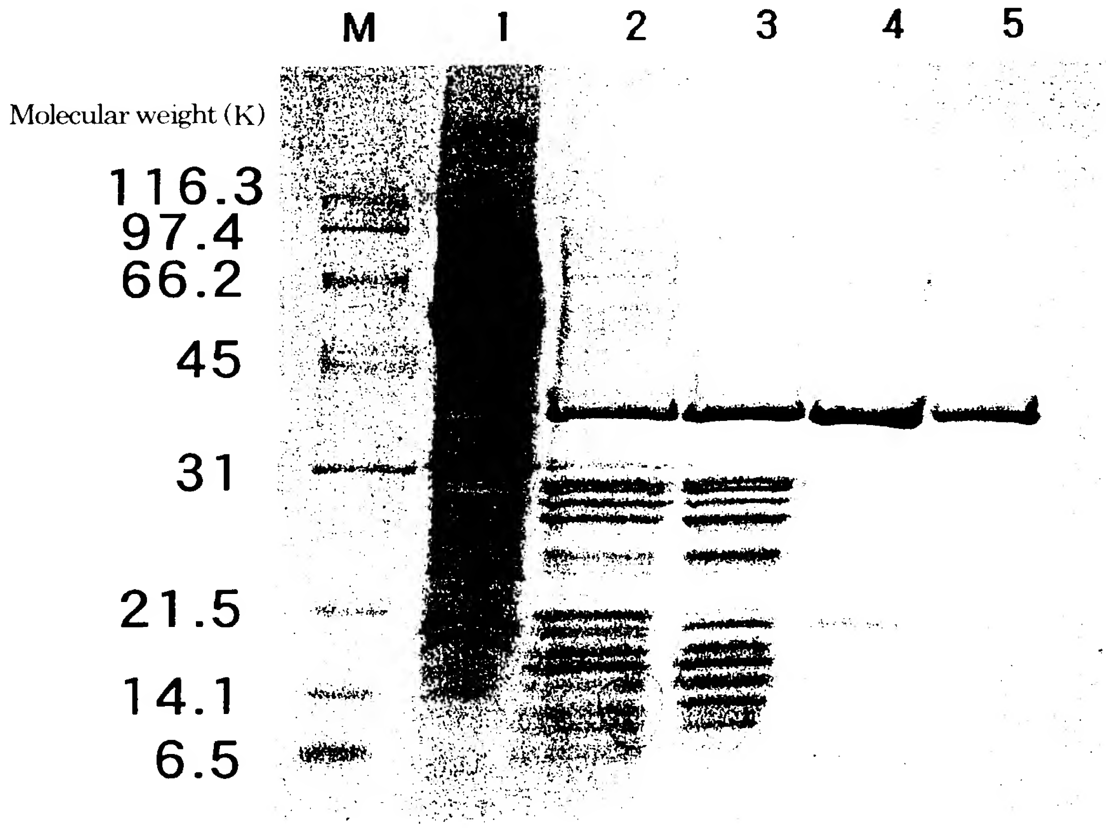


Fig.4

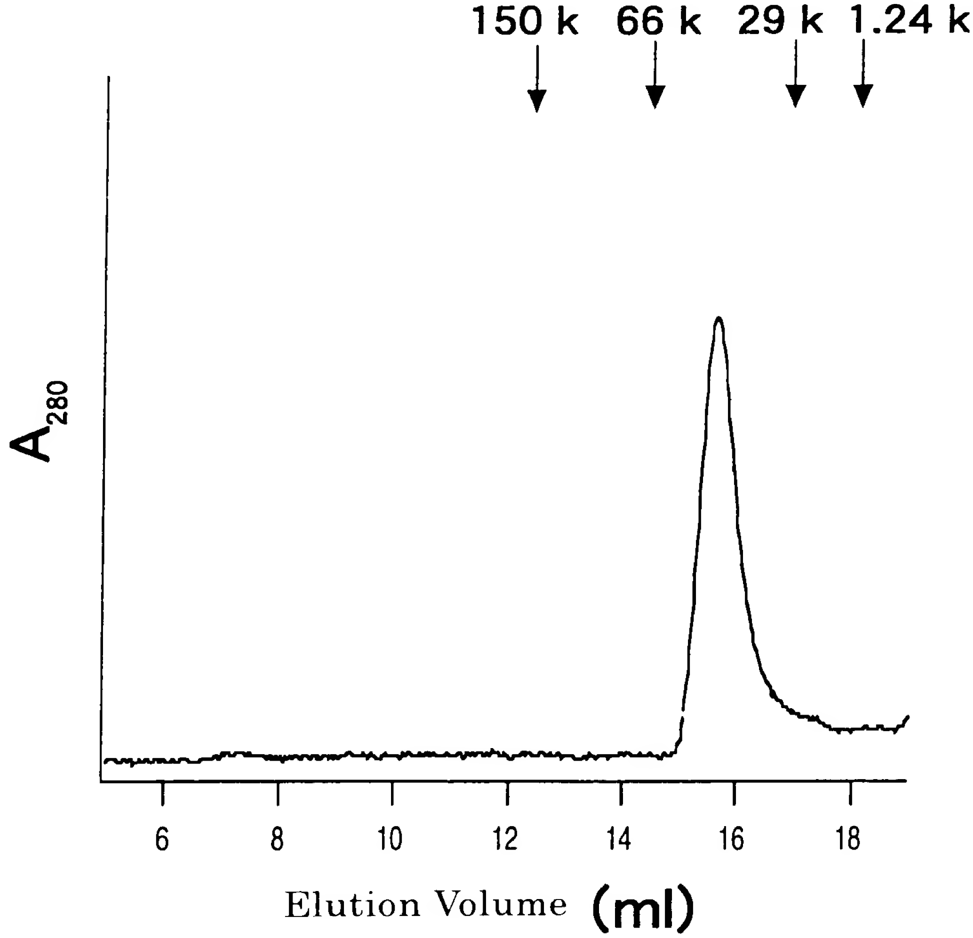


Fig.5

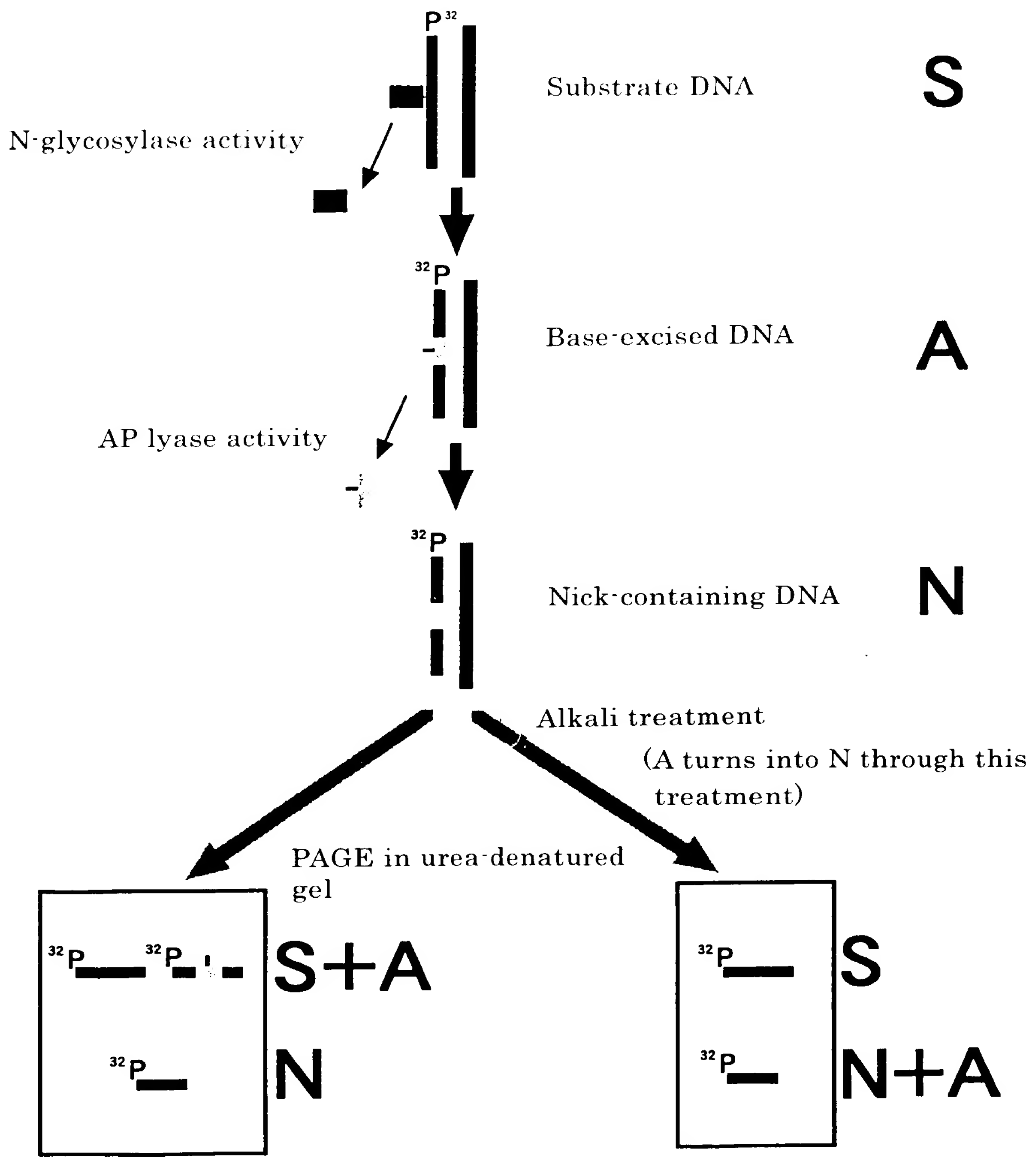
```
Tth MutY       1   MEAWRKALLAWYREN-ARPLPWR---------GE----------KDPYRVLVSEVLLQQTRVEQALPYYRRFL  53
Hsa MutY      51   CDGLARQPEEVVLQASVSSYHLFRDVAEVTAFRGSELSWYDQE-KRDLPWRRRAEDEMDLD-----------RRAYAVWVSEVMLLQTQVATVINYYTGWM 139
Spo MutY       1   MSDSNHFLDLHSYTQLEVERFRESLLQFYDKT-KRILPWRKKECIPPSEDSPLEDWEQPVQRLYEVLVSEIMLQQTRVETVKRYYTKWM  88
Eco MutY       1   MQASQFSAQVLDWYDKYGRKTLPWQ---------ID-----------KTPYKVWLSEVMLQQTQVATVIPYFERFM  56
Eco EndoIII    1   MNKAKRLEILTRLREN--NPHPTT--------ELN----------FSSPFELLIAVLLSAQATDVSVNKATAKLY  55

Tth MutY      54   ERFPTLKALAAASLE-EVLRVWQGAGYYR-RAEHLHRLARSVEEL------PPSFAELR-GLPGLGPYTAAAVASIAFGERVAAVGNVRRVLSRLFARES 145
Hsa MutY     140   QKWPTLQDLASASLE-EVNQLWAGLGYYS-RGRRLQEGARKVVEELGGHMPRTAETLQQLLPGVGRYTAGAIASIAFGQATGVVGNVARVLCRVRAIGA 237
Spo MutY      89   ETLPTLKSCAEAEYNTQVMPLWSGMGFYT-RCKRLHQACGHLAKLHPSEIPRTGDEWAKGIPGVGPYTAGAVLSIAWKQPTGIVGNVIRVLSRALAIHS 187
Eco MutY      57   ARFPTVTDLANAPLD-EVLHLWTGLGYYA-RARNLHKAAQQVATLHGGKFPETFEEVA-ALPGVGRSTAGAILSLSLGKHFPILGNVKRVLARCYAVSG 153
Eco EndoIII   56   PVANTPAAMLELGVE-GVKTYIKTIGLYNSKAENIIKTCRILLEQHNGEVPEDRAALE-ALPGVGRKTANVVLNTAFGWPTIAVTHIFRVCNRTQFAPG 153
                                                                                                          #

Tth MutY     146   -PK----EKELFALAQGLLPEGVDPGVWNQALMELGATVCLPKRPRCGACPLGAFCRG------------KEAPGRYP------APR---------------K 210
Hsa MutY     238   DPSSTLVSQQLWGLAQQLVDP-ARPGDFNQAAMELGATVCTPQRPLCSQCPVESLCRARQRVEQEQLLASGSLSGSPDVEECAPNTGQCHLCLPPSEPWD 336
Spo MutY     188   DCSKGKANALIWKLANELVDP-VRPGDFNQALMELGAITCTPQSPRCSVCPISEICKAYQ---EQNVIRDGNTIKYD---IEDVPCN-ICITDIPS-----K 276
Eco MutY     154   WPGKKEVENKLWSLSEQVTPA-VGVERFNQAMMDLGAMICTRSKPKCSLCPLQNGCIA------------AANSWALYP-----GKK-----------P------K 225
Eco EndoIII  154   -KN----VEQVEEKLLKVVPA-EFKVDCHHWLILHGRYTCIARKPRCGSCIIEDLCEY-------------------------------------------- 205
                                                   *      *  *     *

Tth MutY     211   RRAK----------------EER--LVALVLLGRKG------VHLERLEGR------FQGLYGVPLFPP-EELP--GREAAFGVRS-------------RP-----L 266
Hsa MutY     337   QTLGV----VNFPRKASRKPPREESSATCVLEQPGA----LGAQILLVQRPNSGLLAGLWEFPSVTW-EPSEQLQRKALLQELQRWAGP-----LPATHLRHL 425
Spo MutY     277   EDLQNWVVARYPVHPAKTKQRE-ERALVVIFQKTDPSTKEKFFLIRKRPSAGLLAGLWDFPTIEFGQESWPKDMDAEFQKSIAQWISNDSRSLIKKYQSR 375
Eco MutY     226   QTL----------------PER---TGYFLLLQH-------EDEVLLAQRPPSGLWGGLYCFPQFAD-EES-----LRQWLAQRQ------------IAADNLTQL 287
Eco EndoIII  206   --K-----------------------------------------EKVD

Tth MutY     267   GEVRHALTHRRLR----------------VEVR-GALWEGEGEDPWKRP--LPKLMEKVLRKALP-----------------PLAH-----------------AGVVPLPDA          325
Hsa MutY     426   GEVVHTFSHIKLTYQVYGLALEGQTPVTTVPPGARWLTQEEFHTAAVSTAMKKVFRVYQGQQPGTCMGSKRSQVSSPCSRKKPRMGQQVLDNFFRSHISTDAHSLNSAAQ 535
Spo MutY     376   GRYLHIFSHIRKTSHVFYAIAS----PDIVTNEDFFWISQSDLEHVGMC----ELGLKNYRAALEIKKRK--------VTSLSN---------------FKEPKLTSARRIVTKAEC461
Eco MutY     288   TAFRHTFSHFHLD-----------------IVP---MWLPVSSFTGCMD-----EGNALWYNLAQP-PSVG------LAAPVER---------------LLQQLRTGAPV          350
```

Tth (*Thermus thermophilus* HB8), *Hsa* (*Homo sapiens*), *Spo* (*Schizosaccharomyces pombe*), *Eco* (*Escherichia coli*)

\# Residue essential for N-glycosylase activity * Residues constituting an iron-sulfur cluster

(D)

Fig.6



Detection of AP lyase activity

Detection of N-glycosylase activity and AP lyase activity

Fig.7

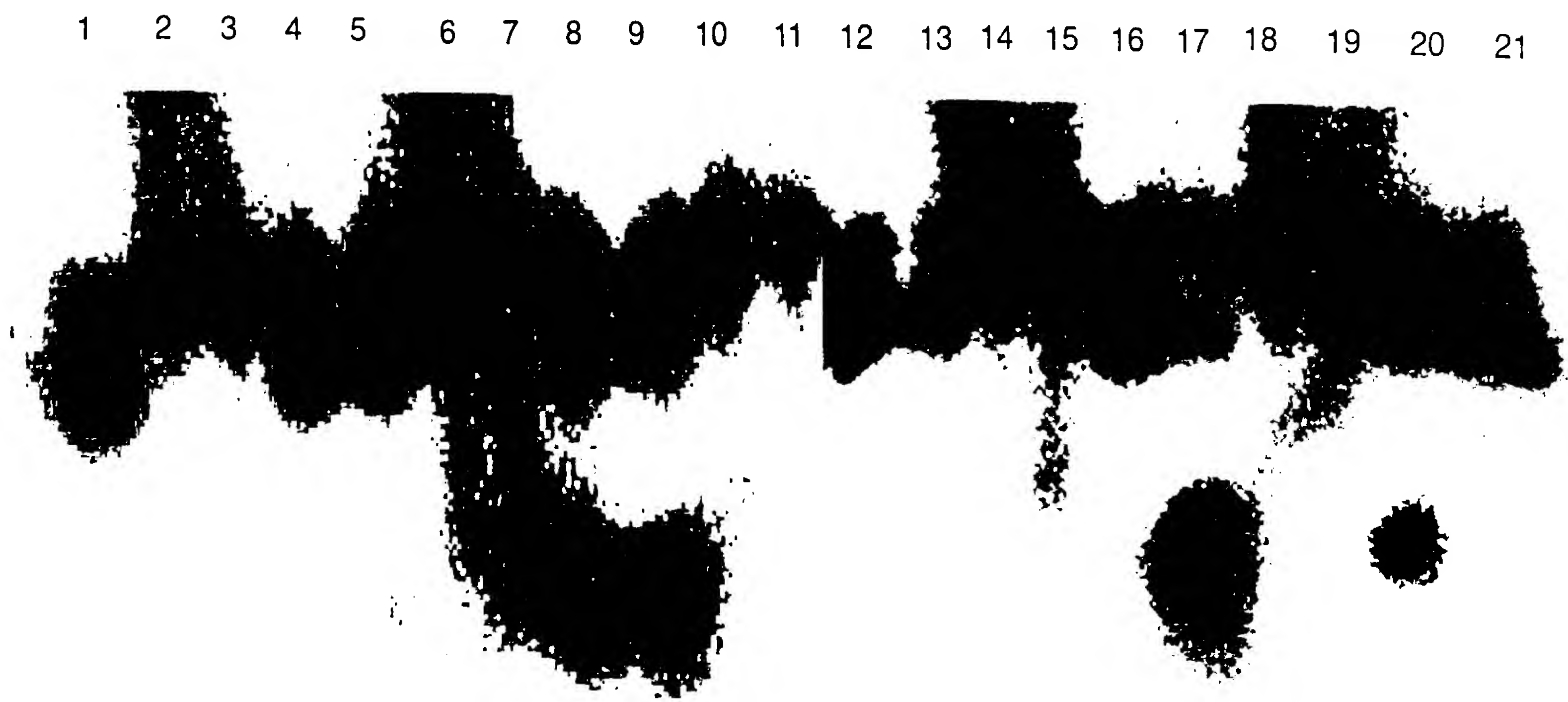


Fig.8

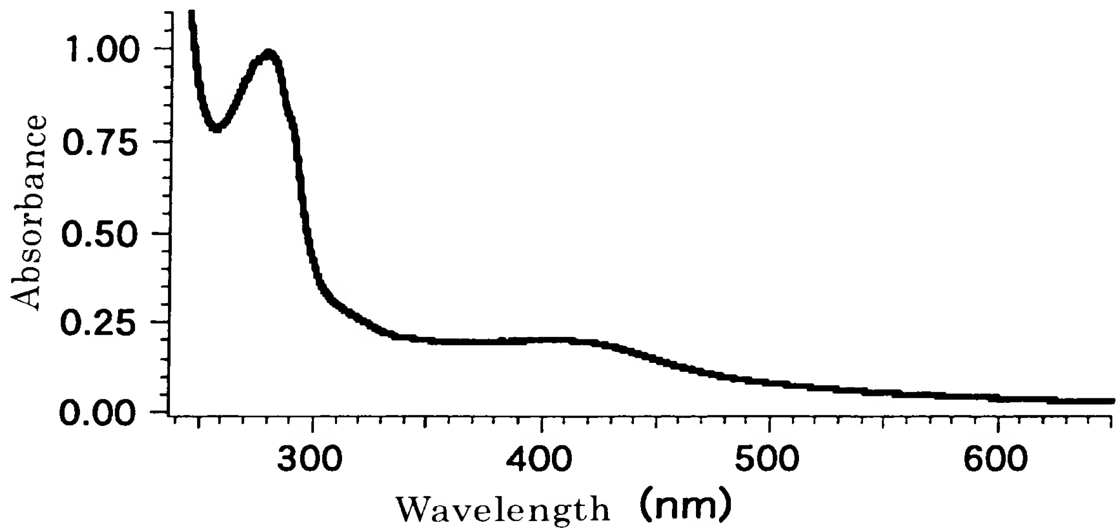

1.00
0.75
0.50
0.25
0.00
Absorbance
300
400
500
600
Wavelength (nm)

Fig.9

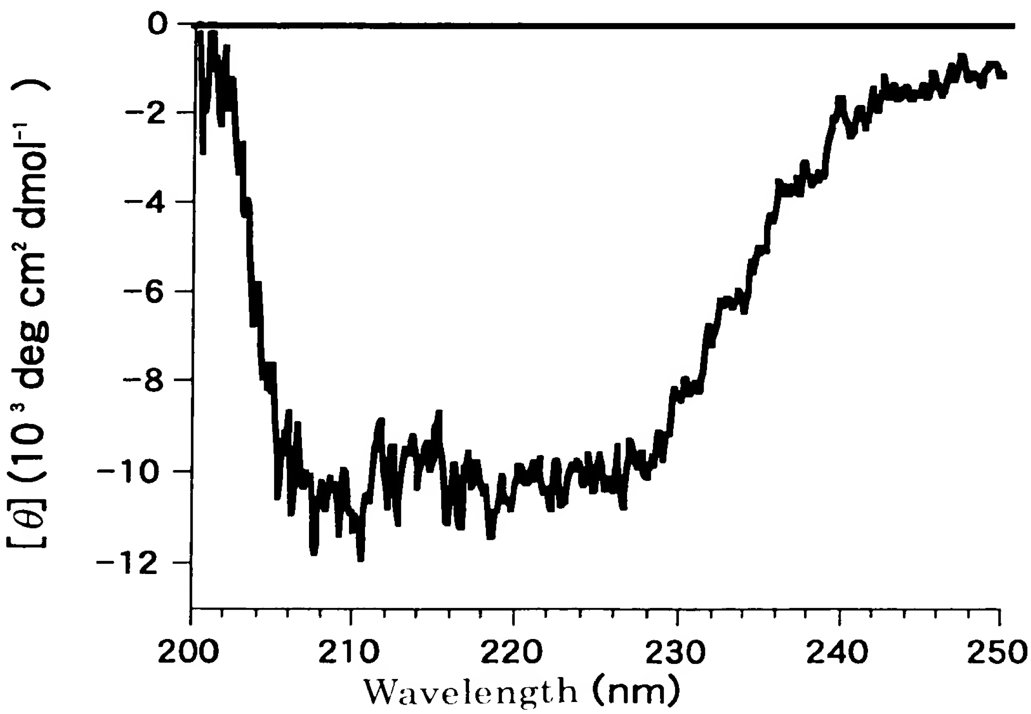
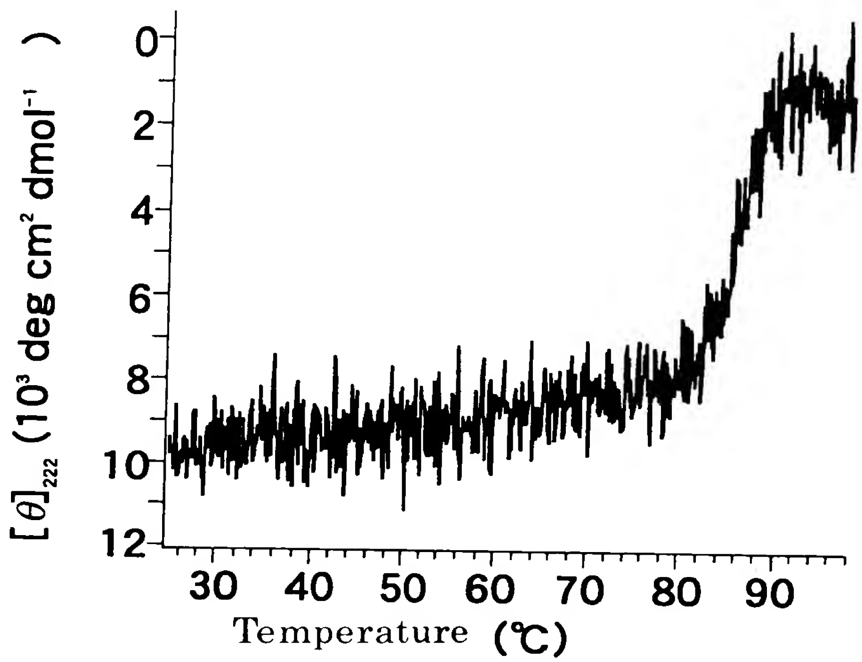

0
−2
−4
−6
−8
−10
−12
[θ] (10³ deg cm² dmol⁻¹)
200
210
220
230
240
250
Wavelength (nm)

Fig.10



$[\theta]_{222}$ (10^3 deg cm^2 dmol^{-1})
0
2
4
6
8
10
12
30
40
50
60
70
80
90
Temperature (℃)

Fig.11

5'-[^{32}P]AGATCTTGACGGGGAAAYCCGAATTCGGCGAACGTGGCGAG-3'
3'-AATCTAGAACTGCCCCTTTXGGCTTAAGCCGCTTGCACCGCTCTT-5'

X : GO, G, C, T　　　Y : A, G

Annealing

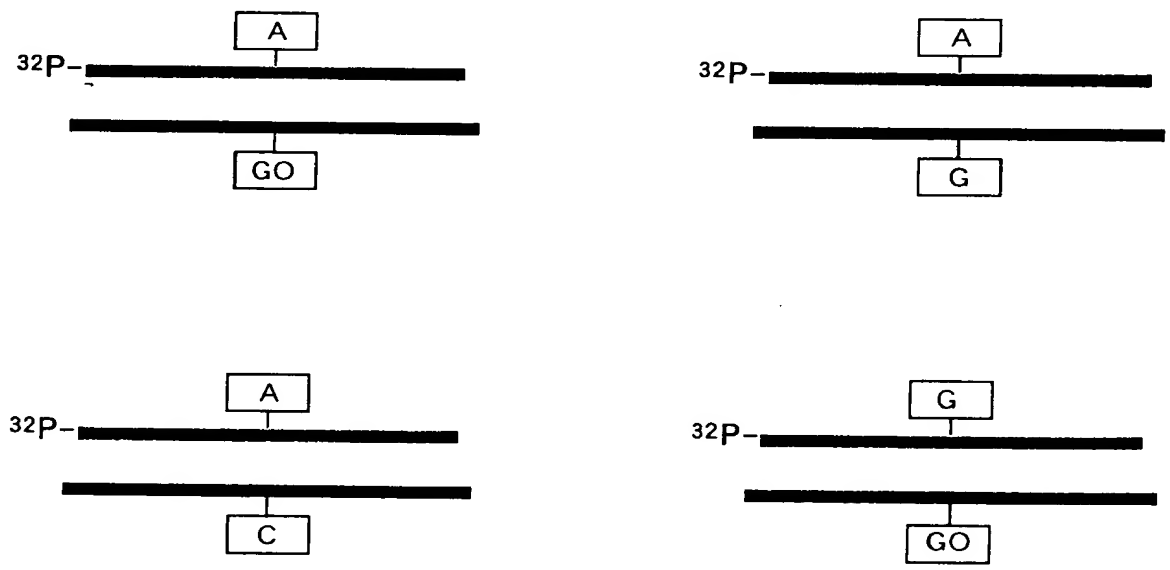
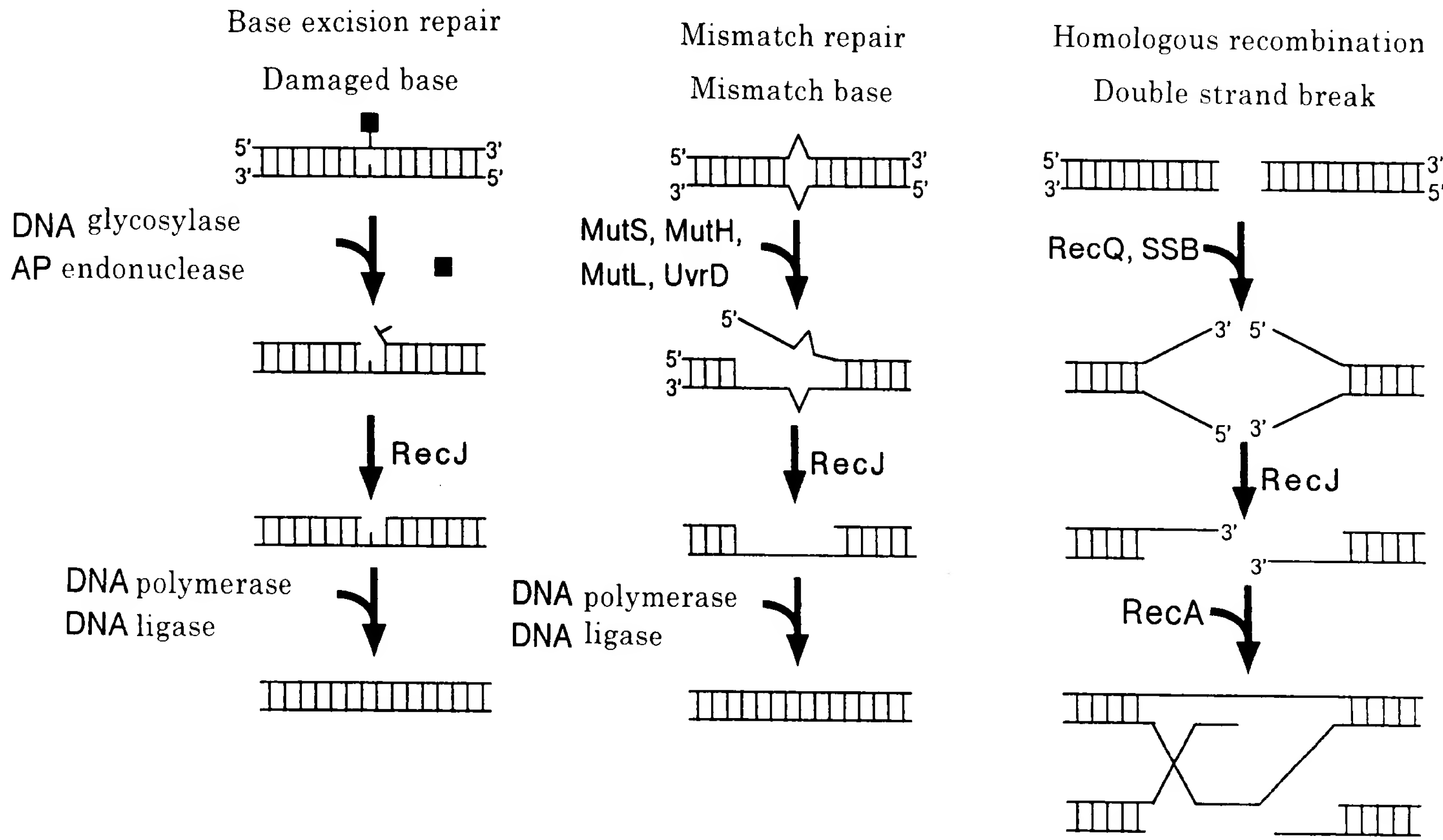


Fig.12



Base excision repair
Damaged base
5'
3'
3'
5'
DNA glycosylase
AP endonuclease
RecJ
DNA polymerase
DNA ligase
Mismatch repair
Mismatch base
5'
3'
3'
5'
MutS, MutH,
MutL, UvrD
5'
5'
3'
RecJ
DNA polymerase
DNA ligase
Homologous recombination
Double strand break
5'
3'
3'
5'
RecQ, SSB
3'
5'
5'
3'
RecJ
3'
3'
RecA

Fig.13

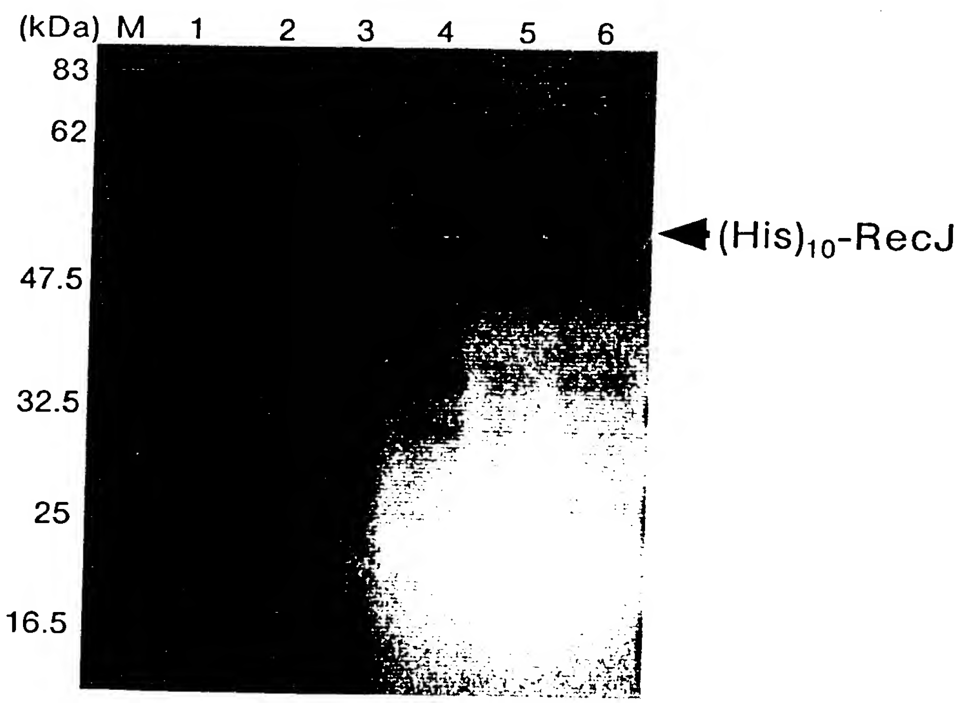
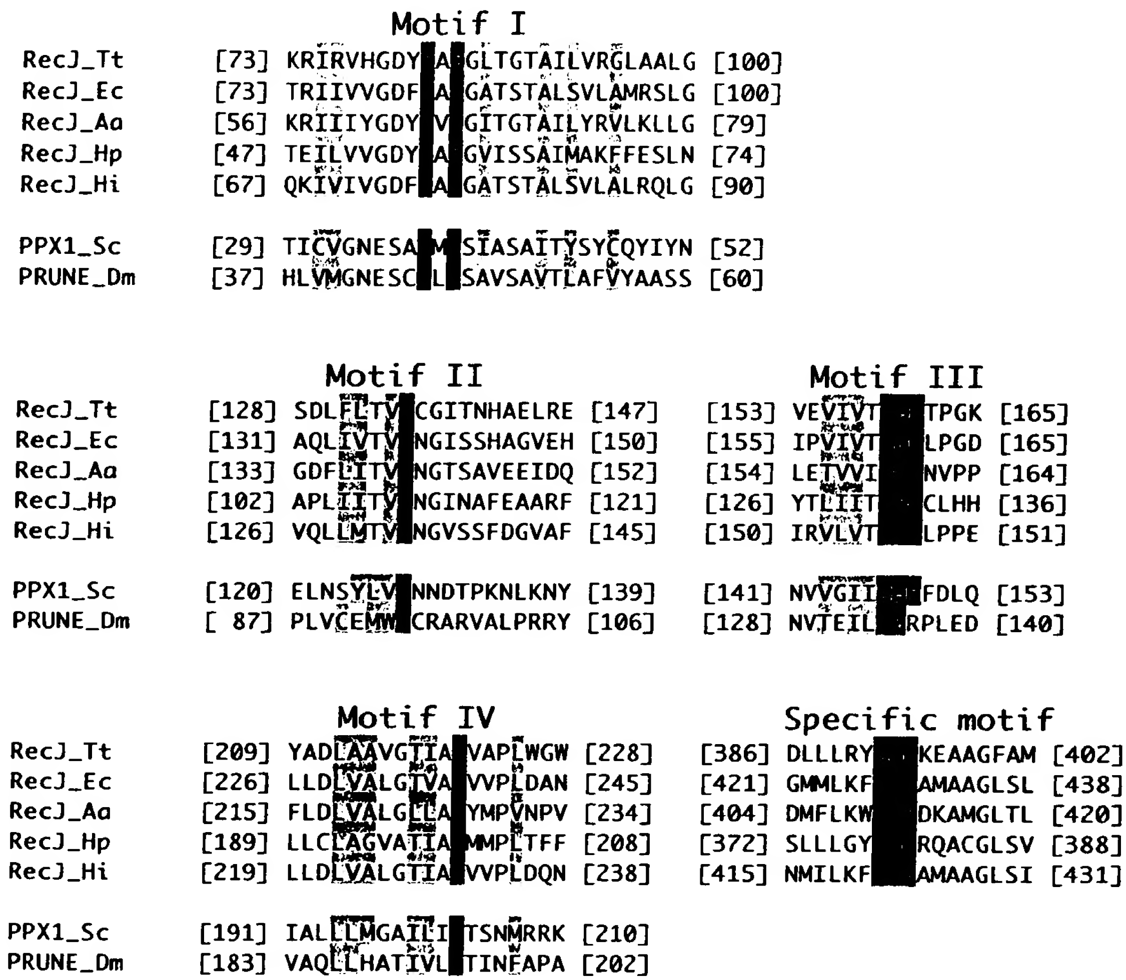


Fig.14



Tt : *Thermus thermophilus* HB8, Ec : *Escherichia coli*, Aa : *Aquifex aeolicus*,
Hp : *Helicobacter pyroli*, Hi : *Haemophilus influenzae* Rd,
Sc : *Saccharomyces cerevisiae*, Dm : *Drosophila melanogaster*

Fig.15

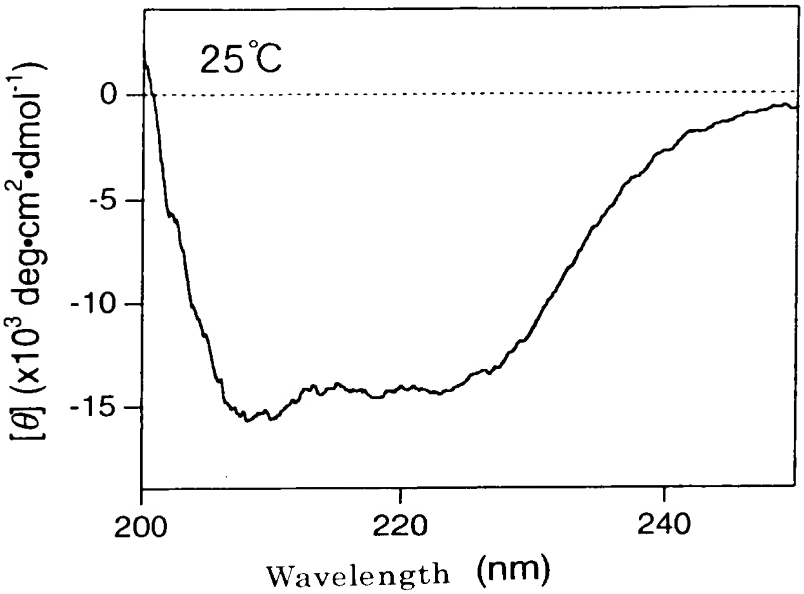

25℃
0
-5
-10
-15
[θ] (x10³ deg•cm²•dmol⁻¹)
200
220
240
Wavelength (nm)

Fig.16

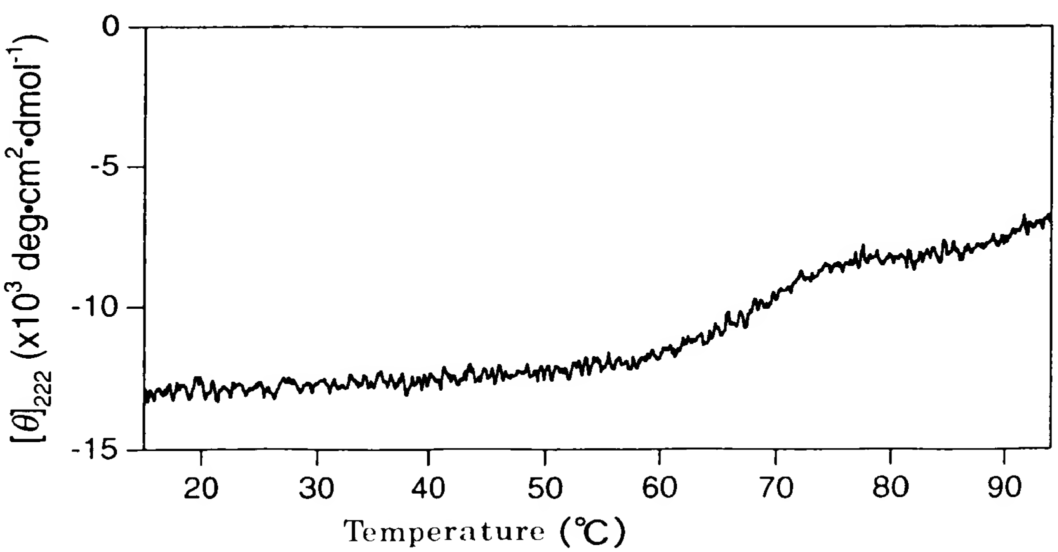

0
-5
-10
-15
[θ]222 (x10³ deg•cm²•dmol⁻¹)
20
30
40
50
60
70
80
90
Temperature (℃)

Fig.17

Substrate DNA : 49-mer ssDNA

5'-ACTACTTGGTACACTGACGCGAGCACGCAGGAGCTCATTCCAGTGCGCA-3'

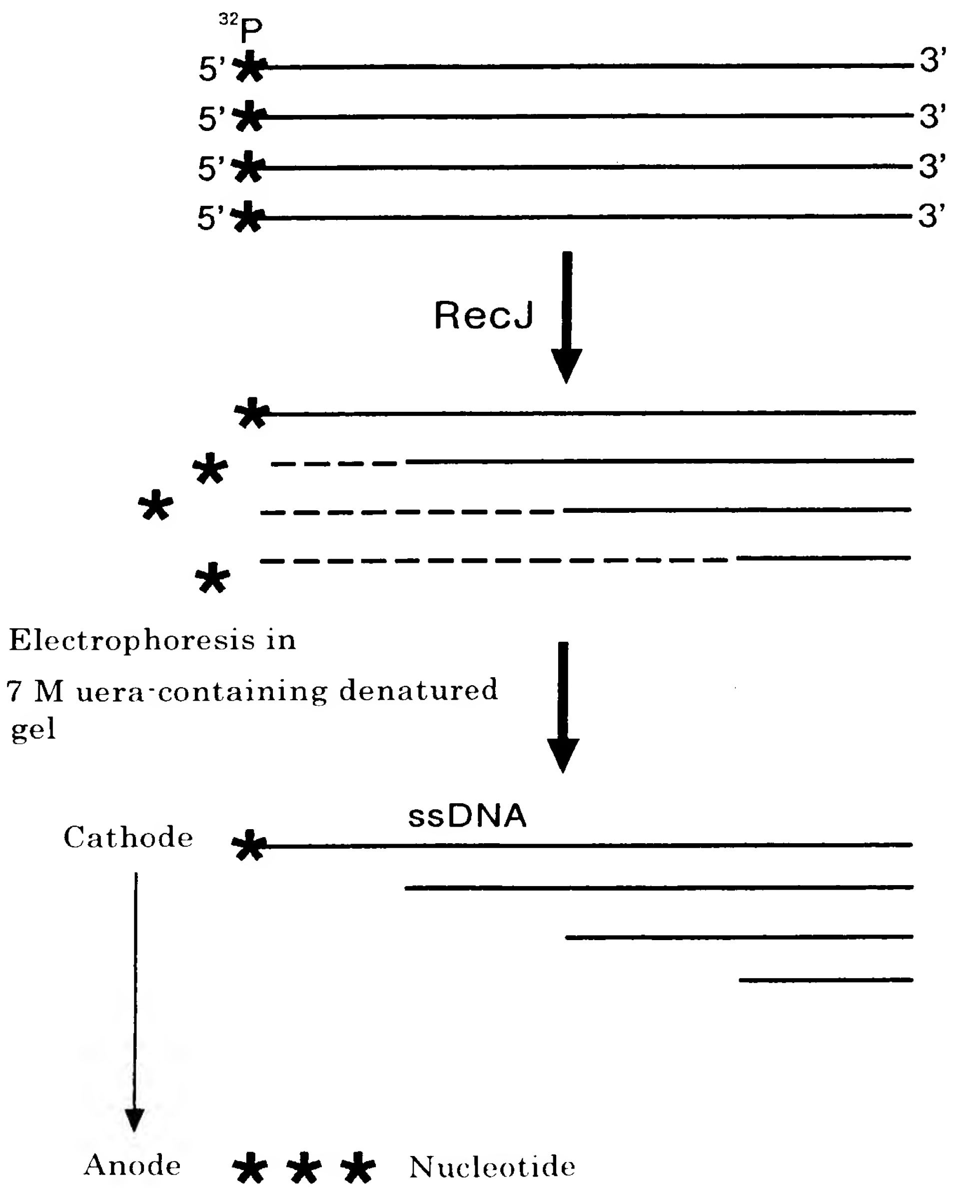
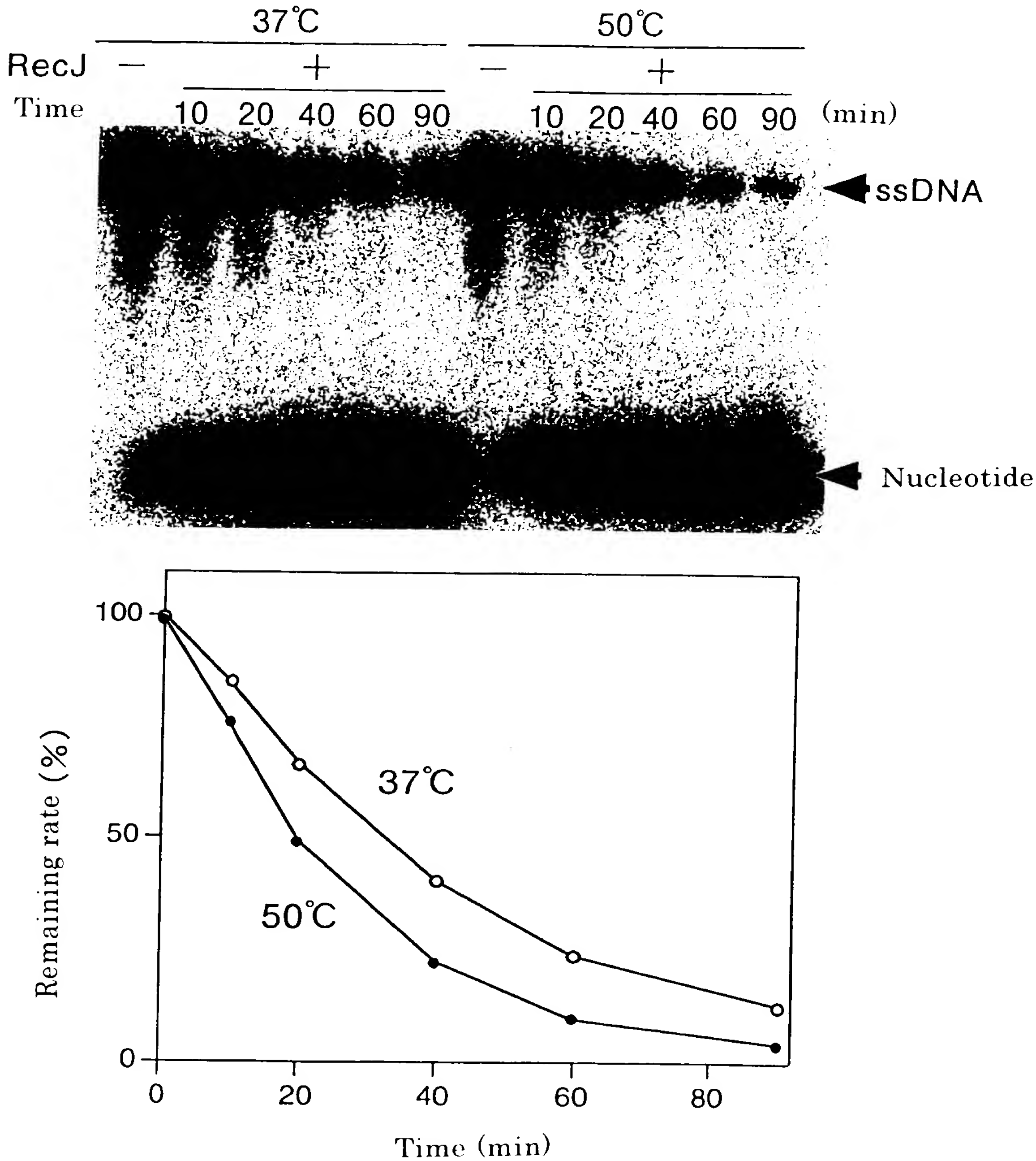


Fig.18



37℃
50℃
RecJ
−
+
−
+
Time
10 20 40 60 90
10 20 40 60 90
(min)
ssDNA
Nucleotide
100
50
0
Remaining rate (%)
37℃
50℃
0
20
40
60
80
Time (min)

Fig.19

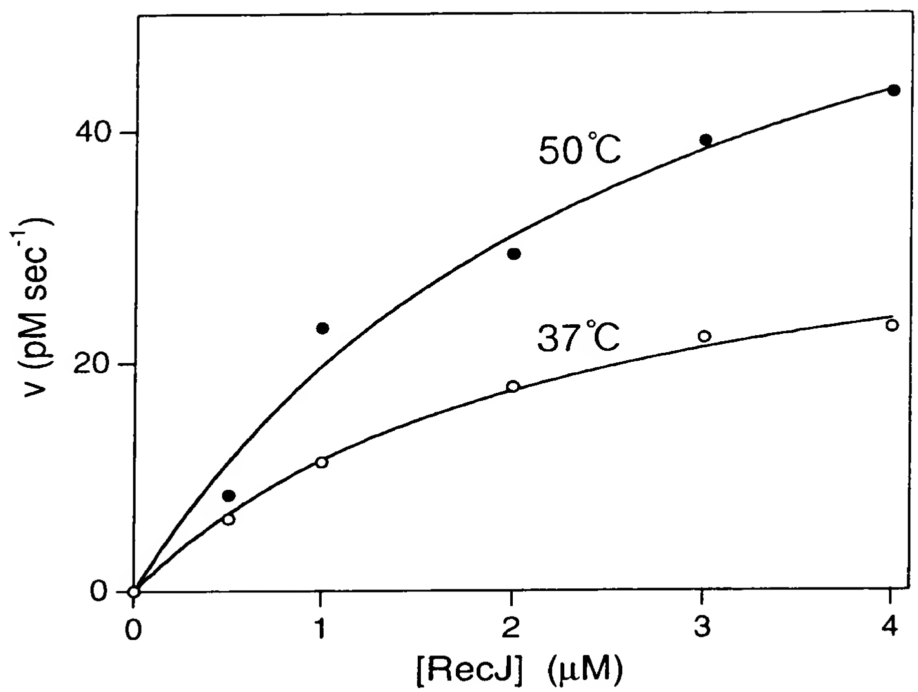


Fig.20

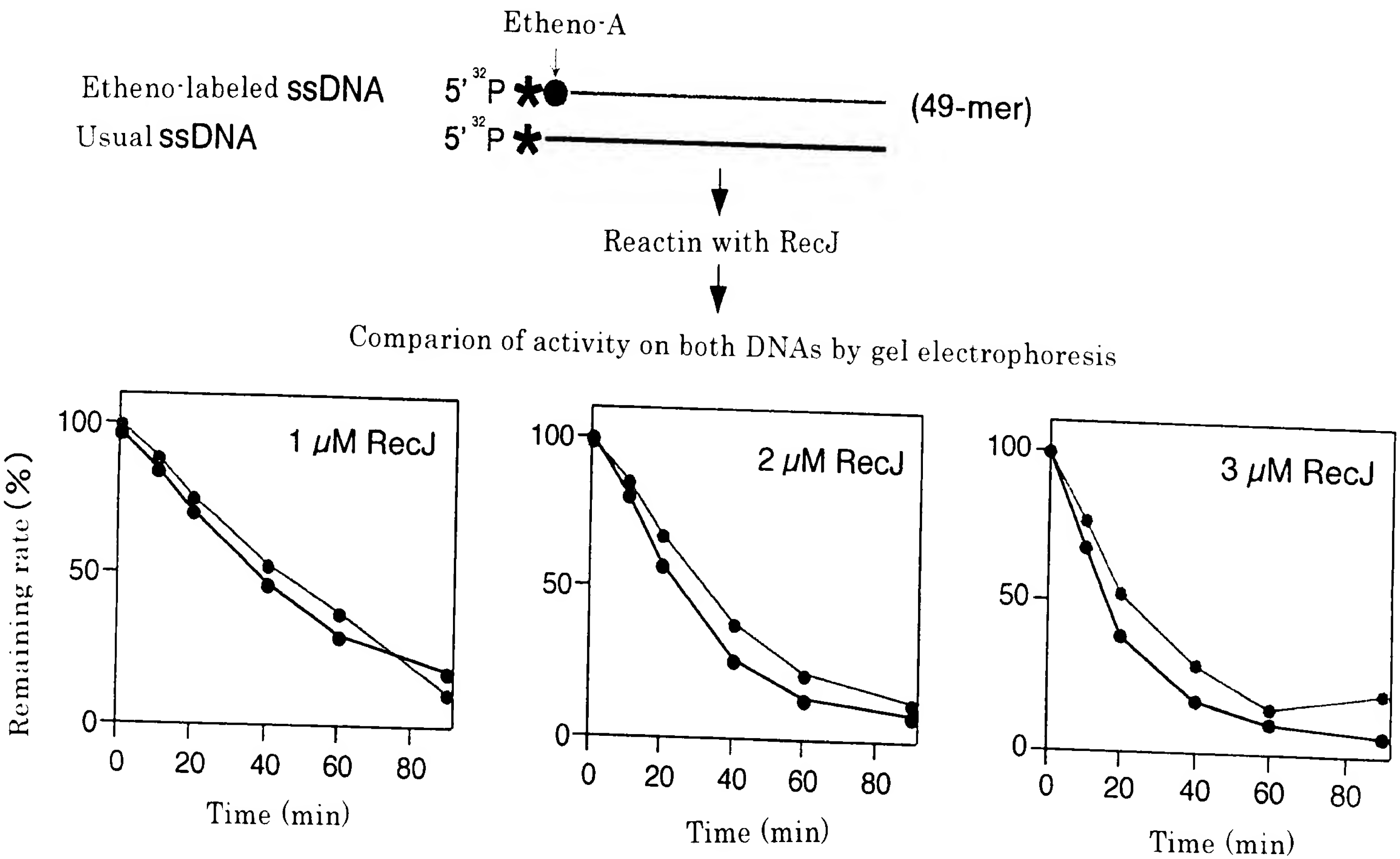
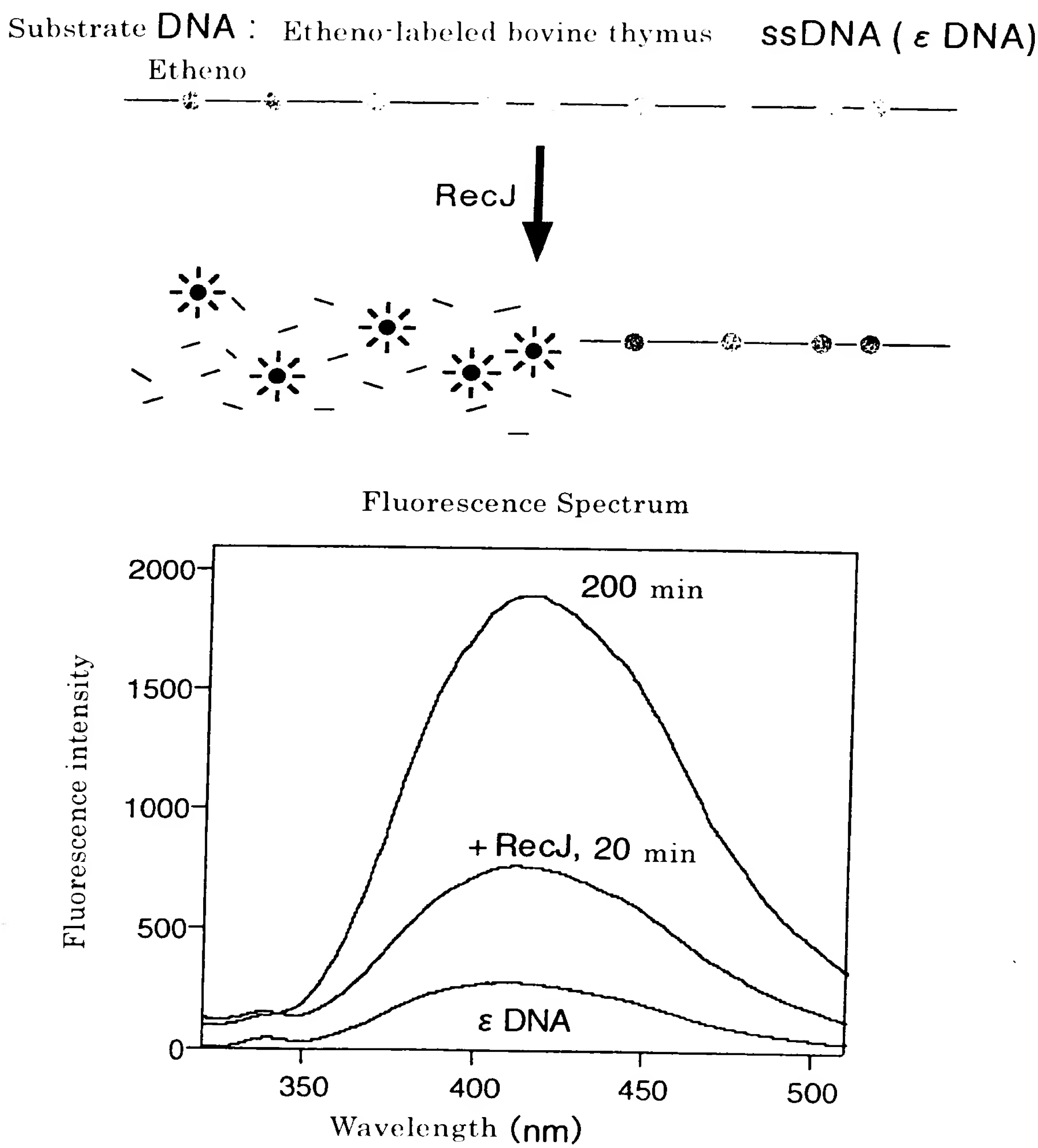
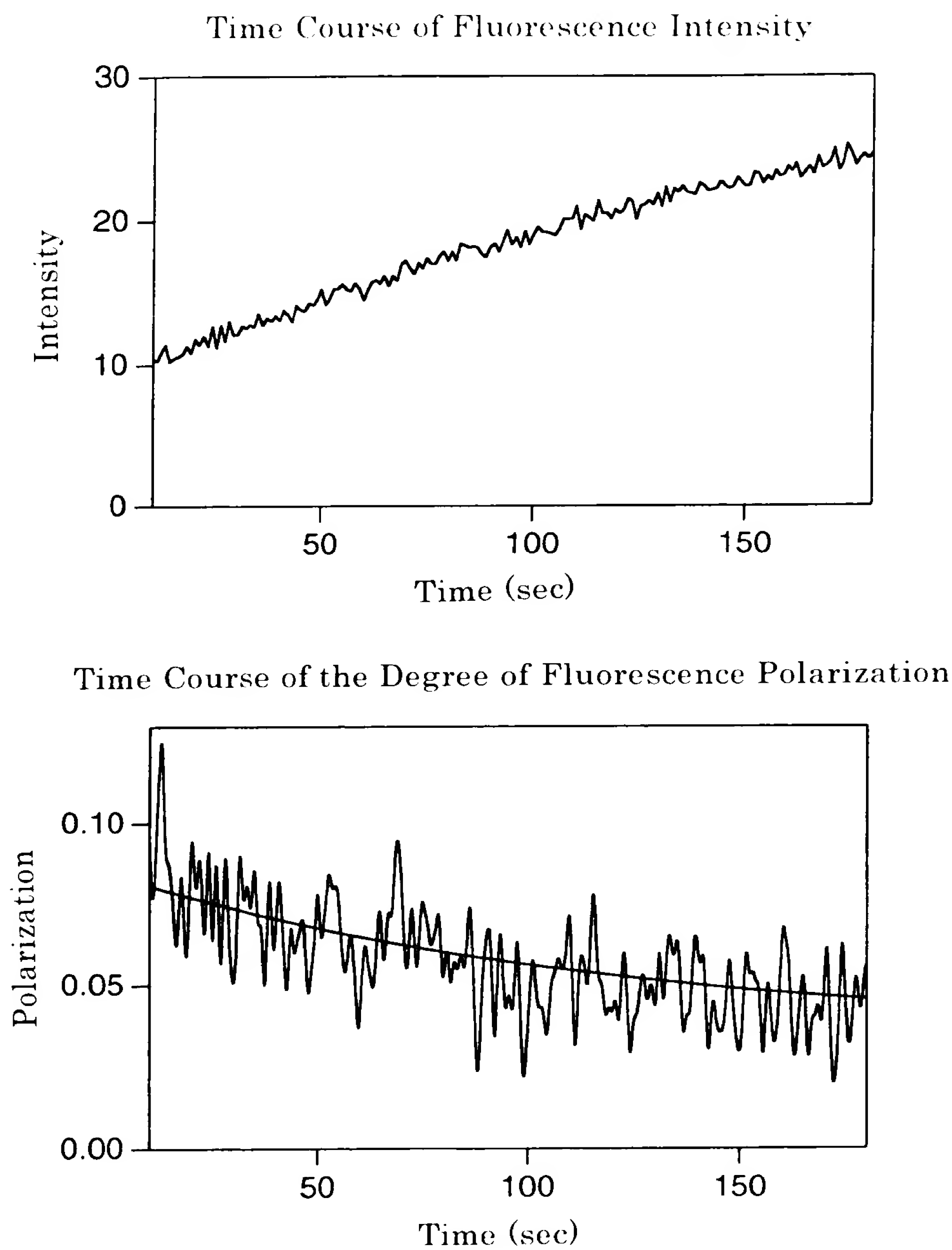

Etheno-A
Etheno-labeled ssDNA
Usual ssDNA
5' ^{32}P
5' ^{32}P
(49-mer)
Reactin with RecJ
Comparion of activity on both DNAs by gel electrophoresis
Remaining rate (%)
1 μM RecJ
2 μM RecJ
3 μM RecJ
Time (min)
Time (min)
Time (min)
0
50
100
0
20
40
60
80

Fig.21



Substrate DNA : Etheno-labeled bovine thymus ssDNA (ε DNA)
Etheno
RecJ
Fluorescence Spectrum
Fluorescence intensity
2000
1500
1000
500
0
200 min
+ RecJ, 20 min
ε DNA
350
400
450
500
Wavelength (nm)

Fig.22



Time Course of Fluorescence Intensity
30
20
10
0
Intensity
50
100
150
Time (sec)
Time Course of the Degree of Fluorescence Polarization
0.10
0.05
0.00
Polarization
50
100
150
Time (sec)

Fig.23

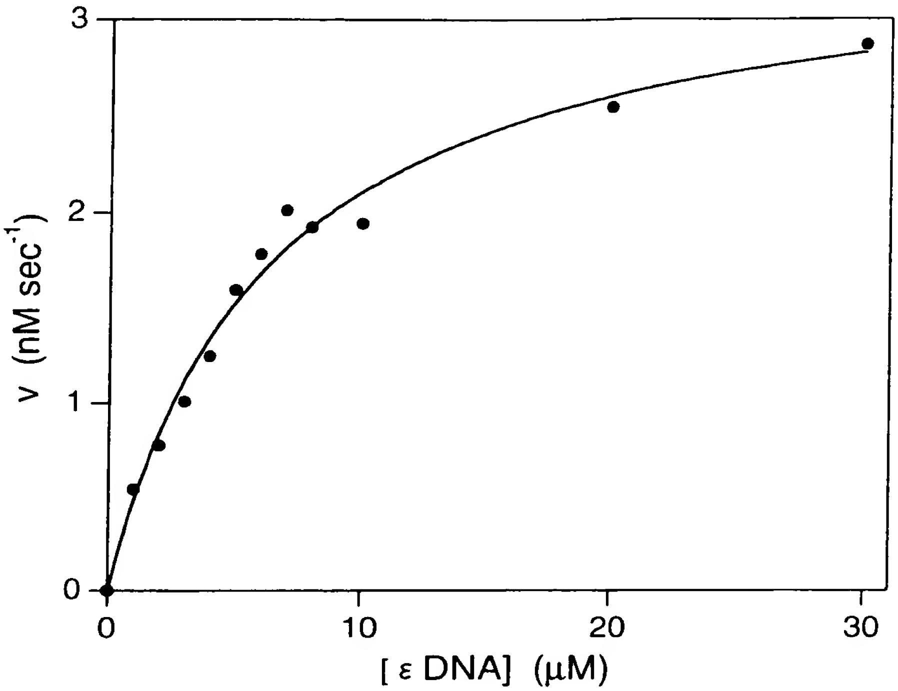


Fig.24

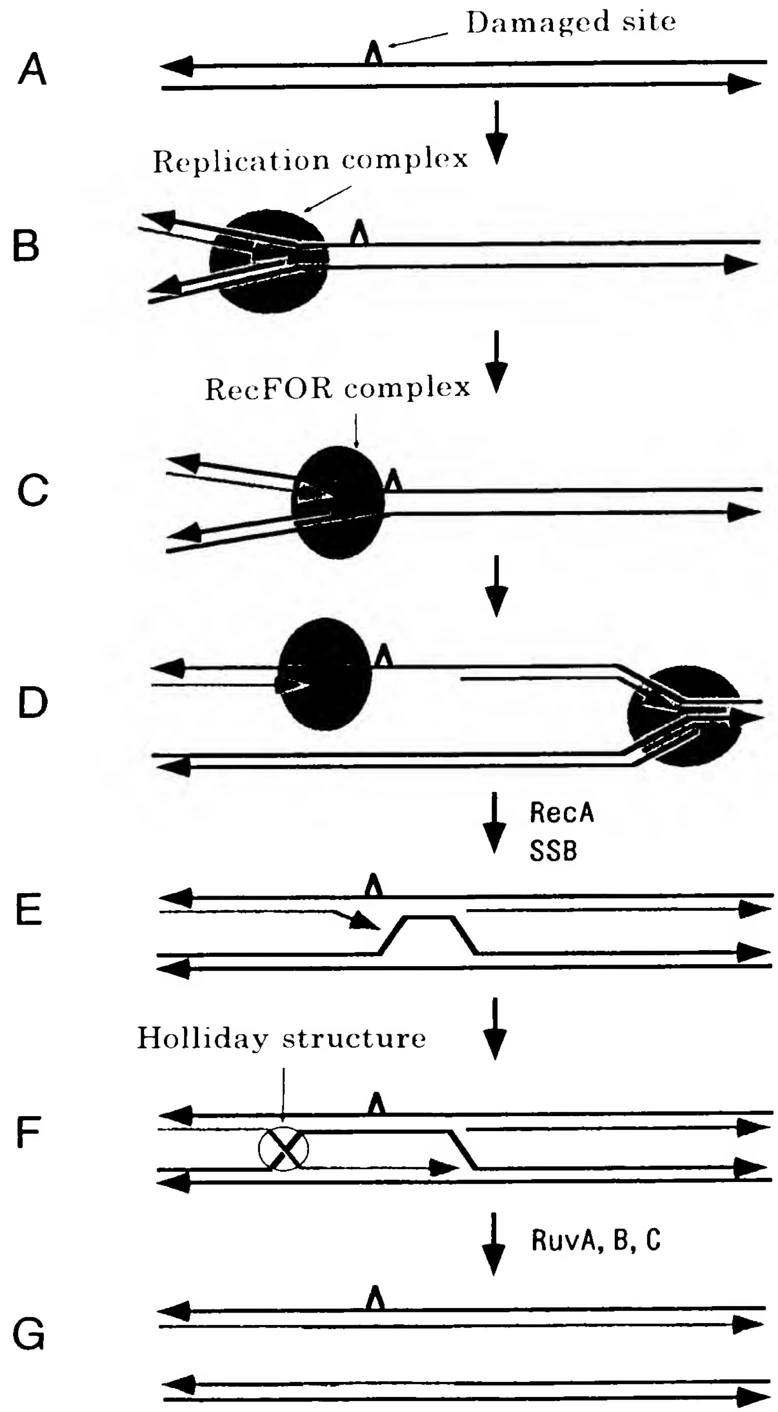

Damaged site
A
Replication complex
B
RecFOR complex
C
D
RecA
SSB
E
Holliday structure
F
RuvA, B, C
G

Fig.25

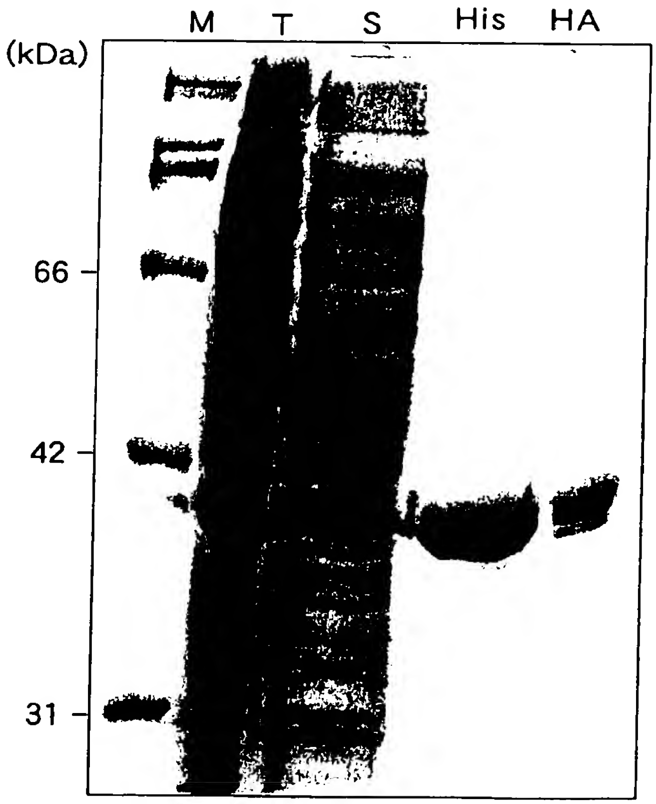


Fig.26

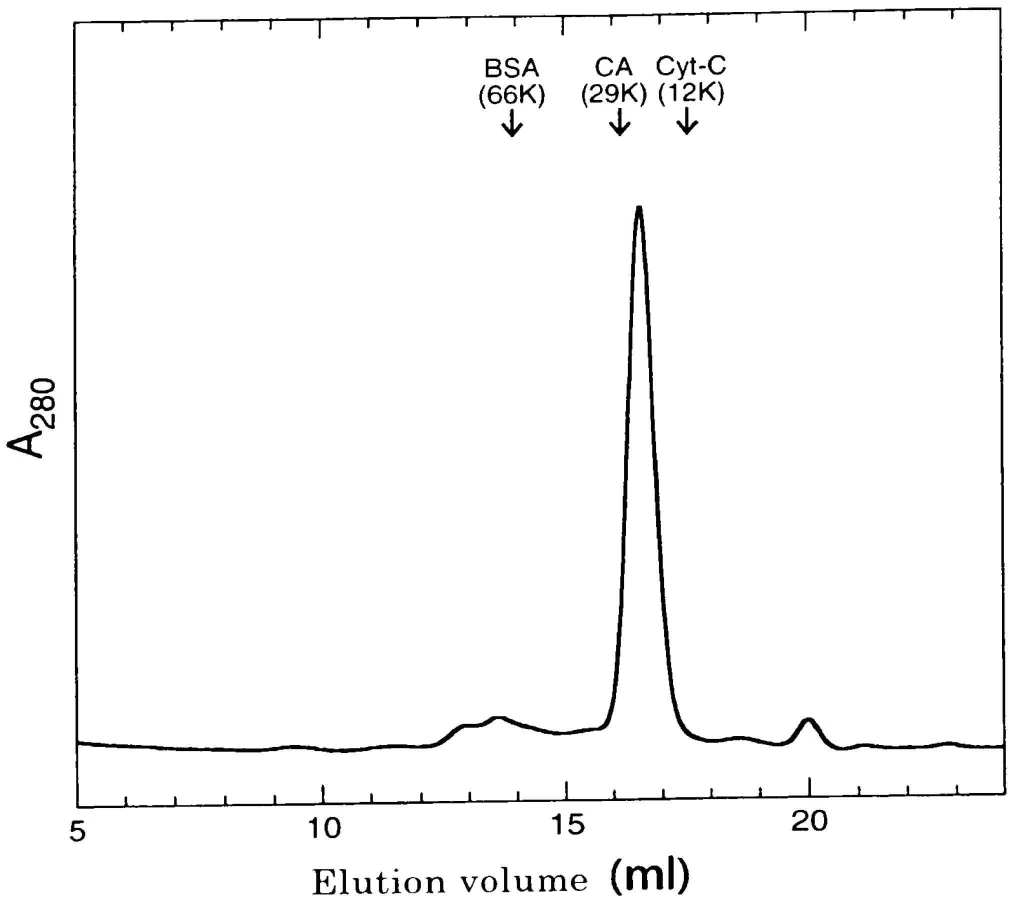
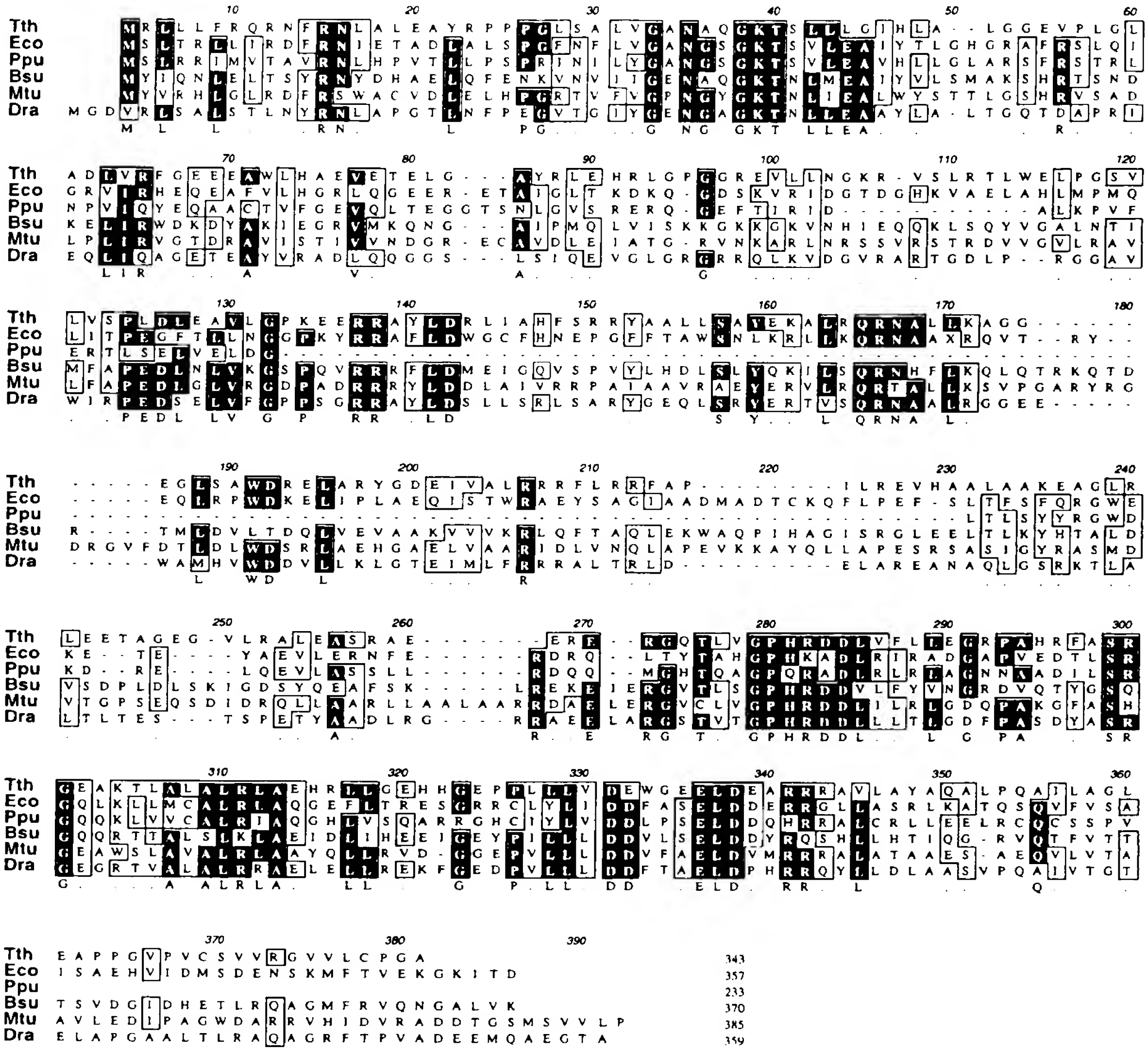


Fig.27



Tth: *Thermus thermophilus* HB8

Eco: *Escherichia coli*

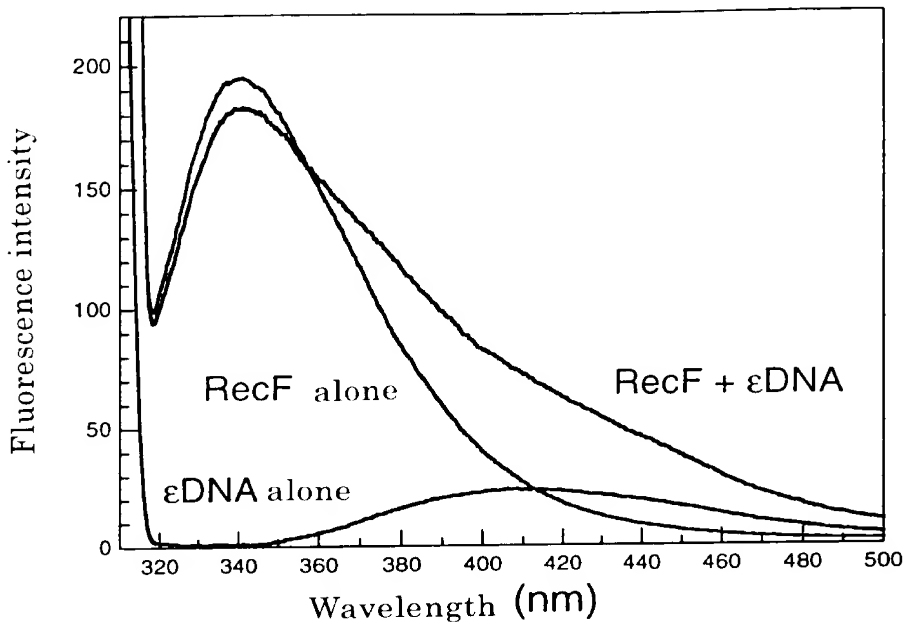
Ppu: *Pseudomonas putida*

Bsu: *Bacillus subtilis*

Mtu: *Mycobacterium tuberculosis*

Dra: *Deinococcus radiodurans*

Fig.28


Fluorescence intensity
200
150
100
50
0
RecF alone
RecF + εDNA
εDNA alone
320
340
360
380
400
420
440
460
480
500
Wavelength (nm)

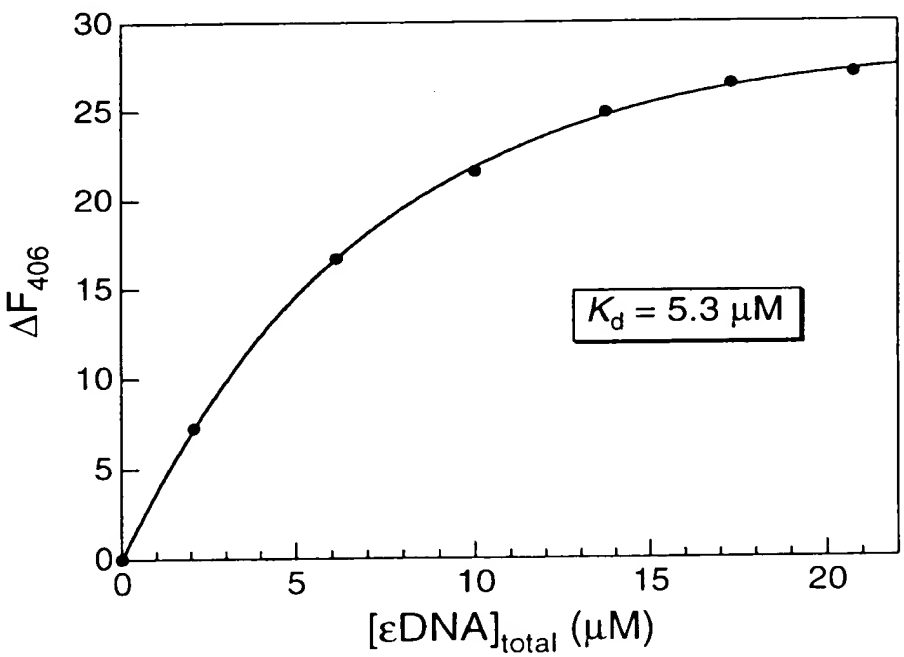
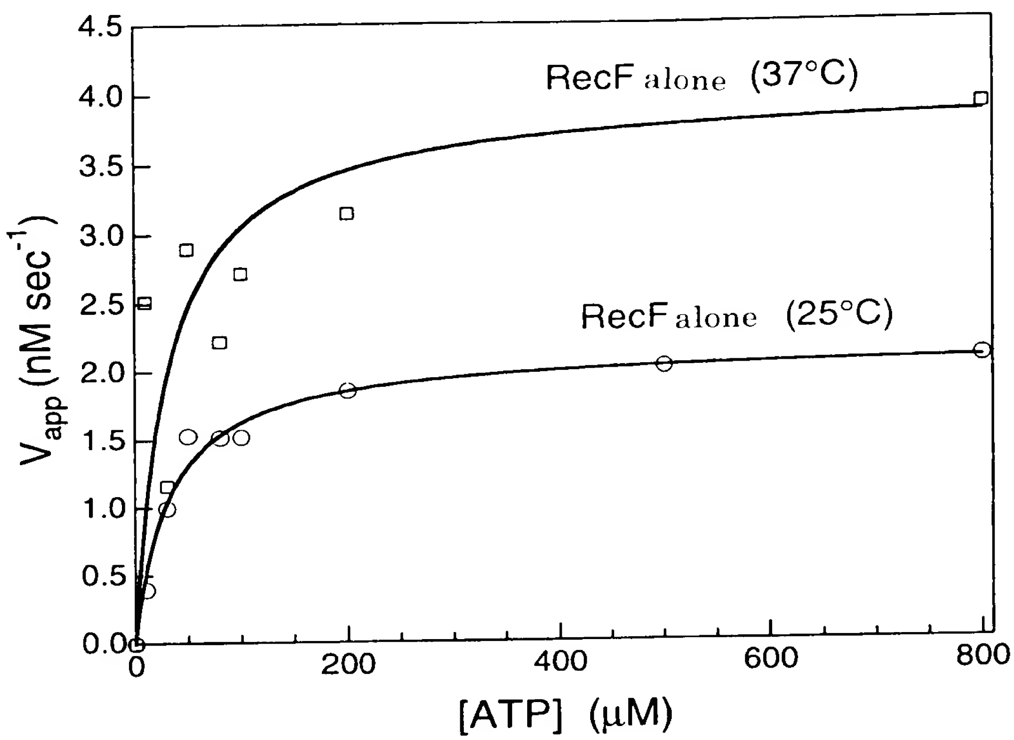
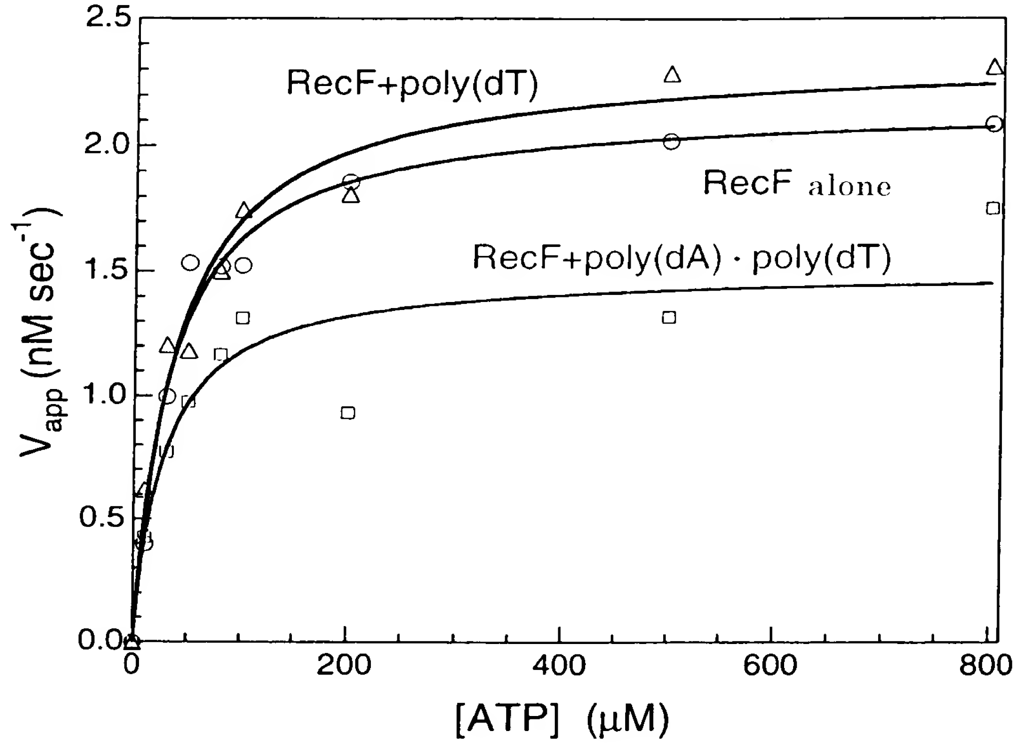

30
25
20
15
10
5
0
ΔF406
Kd = 5.3 μM
0
5
10
15
20
[εDNA]total (μM)

Fig.29



RecF alone (37°C)
RecF alone (25°C)
V_{app} (nM sec^{-1})
[ATP] (μM)
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
200
400
600
800

Fig.30



RecF+poly(dT)
RecF alone
RecF+poly(dA) · poly(dT)
V_{app} (nM sec^{-1})
[ATP] (μM)
2.5
2.0
1.5
1.0
0.5
0.0
0
200
400
600
800

Fig.31

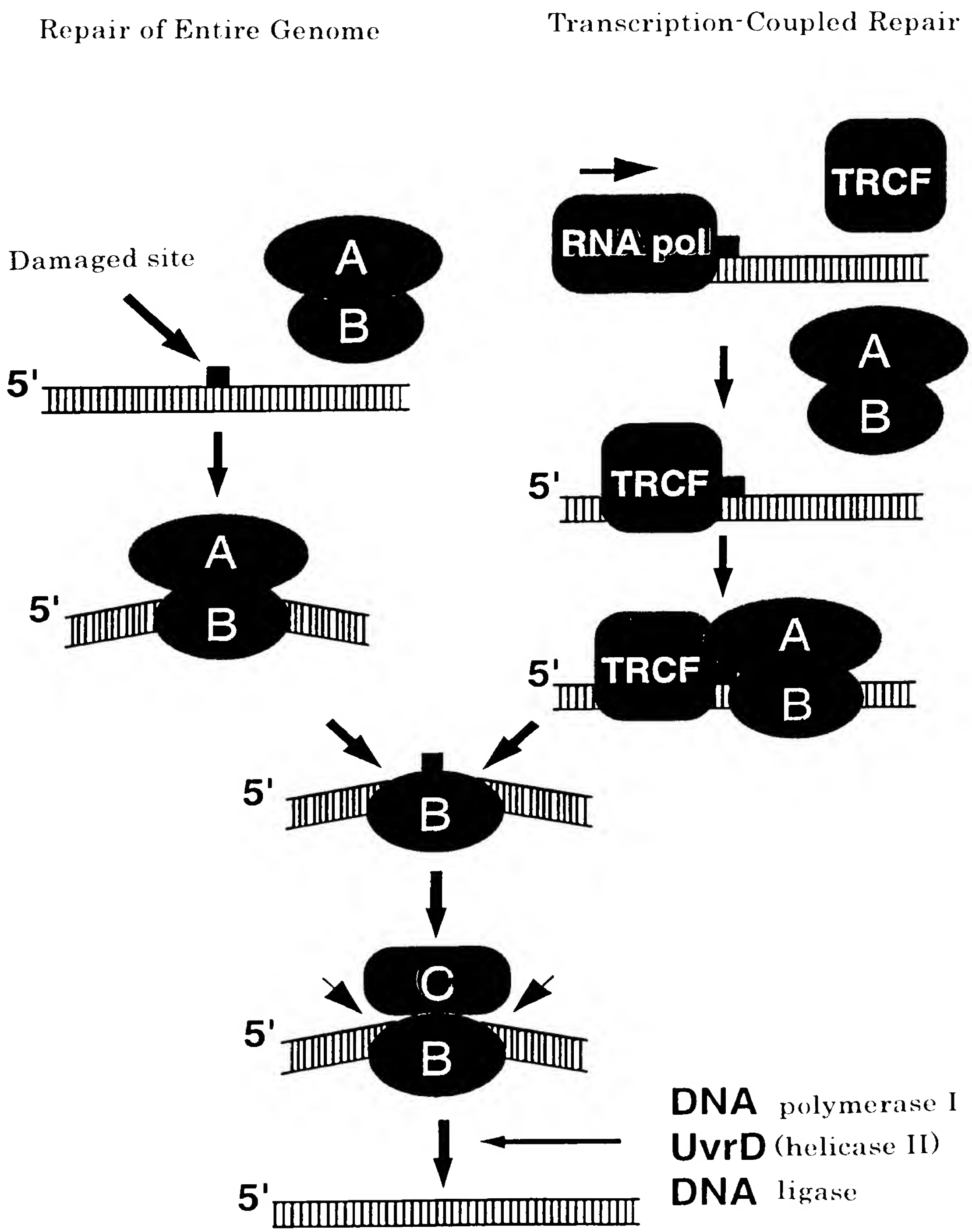

Repair of Entire Genome
Transcription-Coupled Repair
Damaged site
A
B
5'
RNA pol
TRCF
C
DNA polymerase I
UvrD (helicase II)
DNA ligase

Fig.32

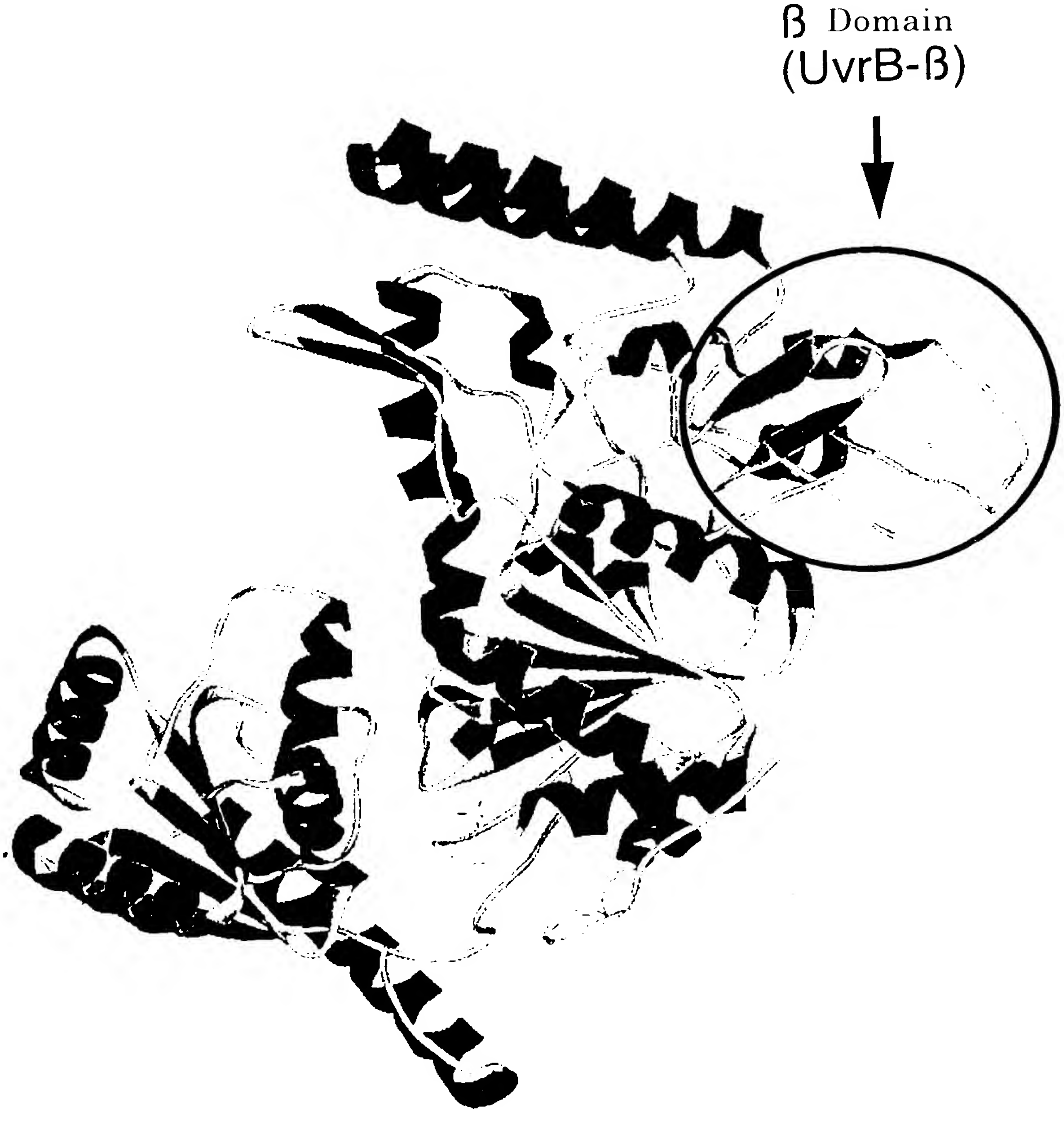
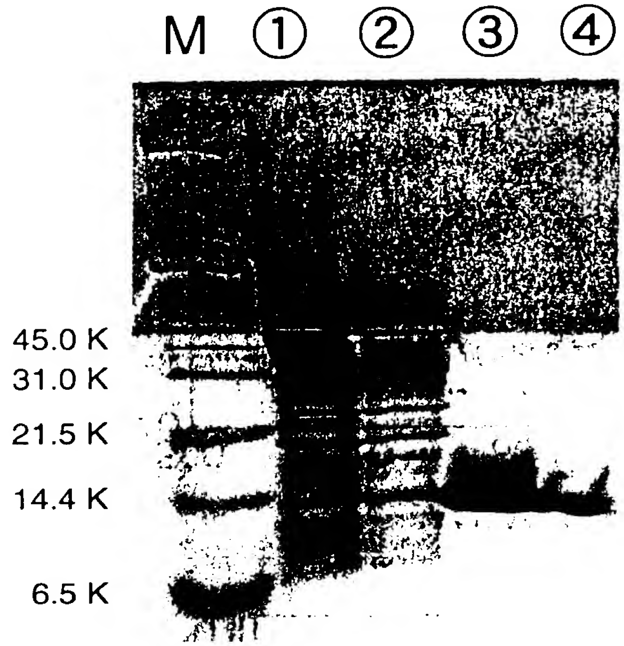


Fig.33

UvrB-ß



TRCF-ß

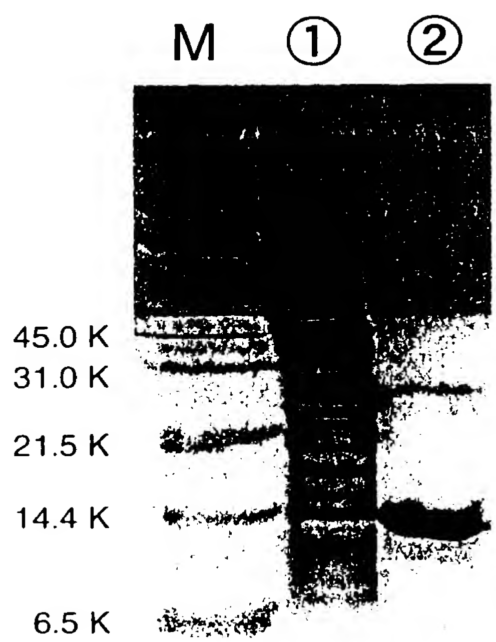
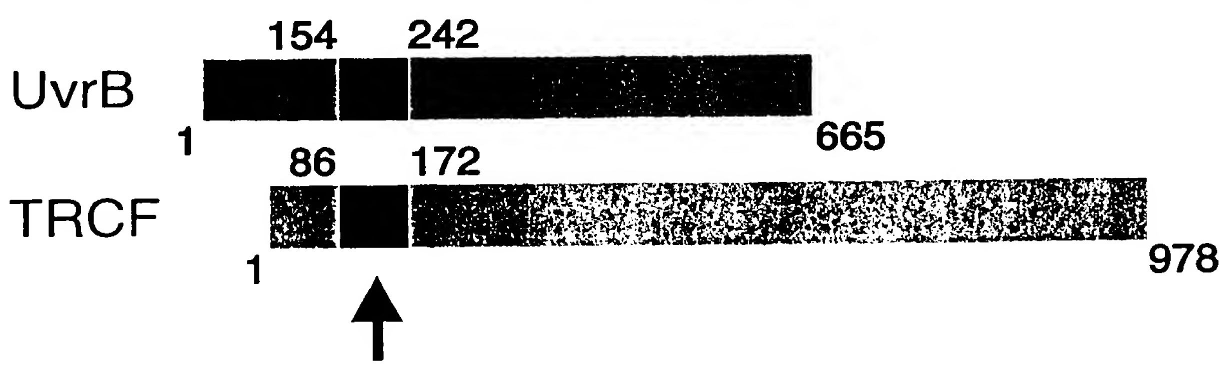


Fig.34

```
UvrB-β  154 RNLVVERGKPYPREVLLERLLELGYQRNDI 184
TRCF-β   86 WRLLLEVGRAYPREALLSRLLKLGYAR--- 113
              *..* *. **** ** *** *** *

UvrB-β  185 DLSPGRFRAKGEVLEIFPAYETEPIRVELF 215
TRCF-β  114 DED---YRVLGEVVELG------EVRLEFF 148
            *     .*  ***.*.        .*.* *

UvrB-β  216 GDEVERISQVHPVTG-ERLRELPG------ 236
TRCF-β  149 GDELERLVVRGEERRRHVLLPKPGKAEGFT 163
            ***.**            *   **

UvrB-β  237 ---FVLFPA 242
TRCF-β  164 SKKVLHEPG 172
                . **
```

* Identical amino acid residues

. Homologous amino acid residues



Homologous region

Fig.35

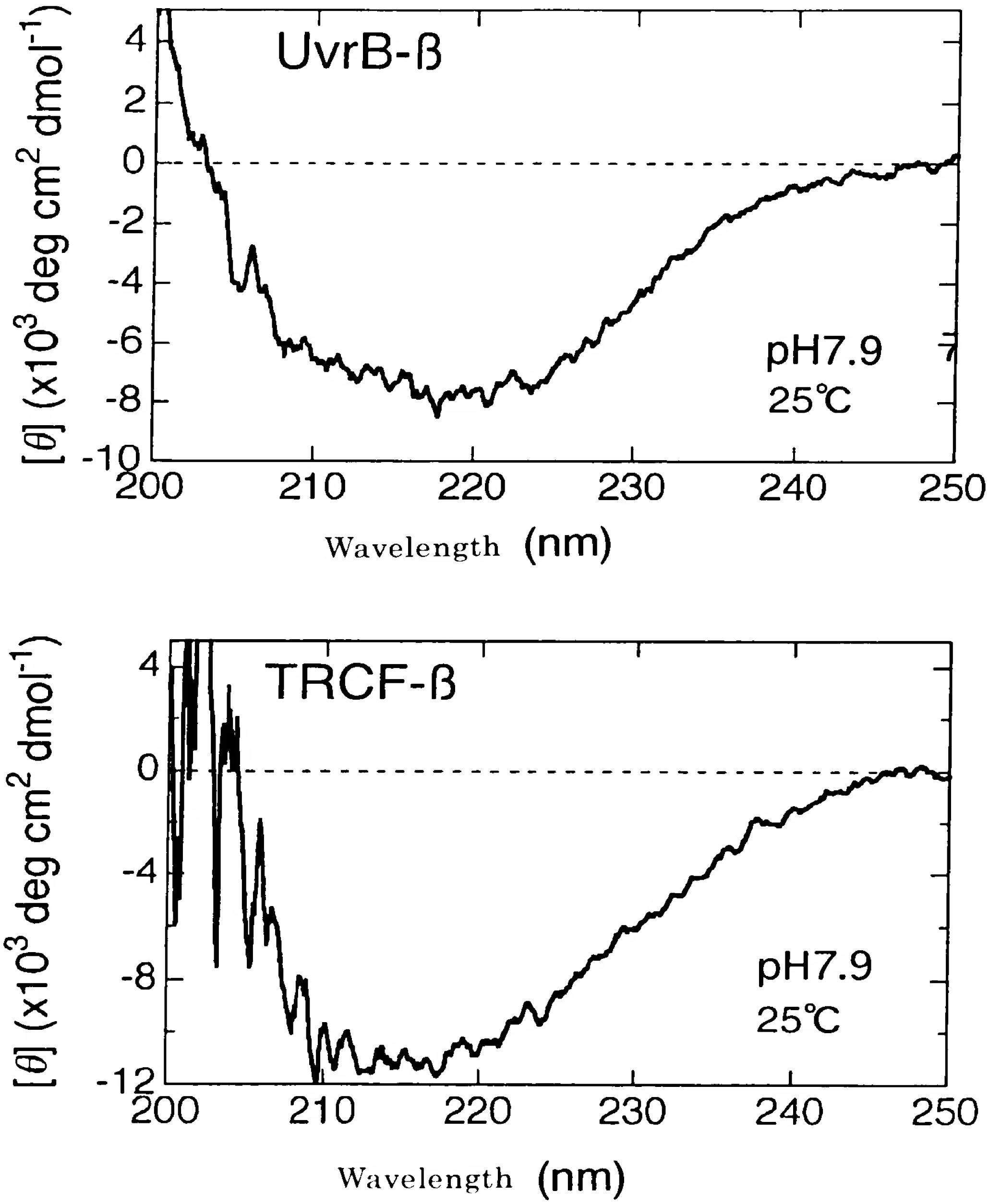

UvrB-β
pH7.9
25℃
[θ] (x10³ deg cm² dmol⁻¹)
4
2
0
-2
-4
-6
-8
-10
200
210
220
230
240
250
Wavelength (nm)
TRCF-β
pH7.9
25℃
[θ] (x10³ deg cm² dmol⁻¹)
4
0
-4
-8
-12
200
210
220
230
240
250
Wavelength (nm)

Fig.36

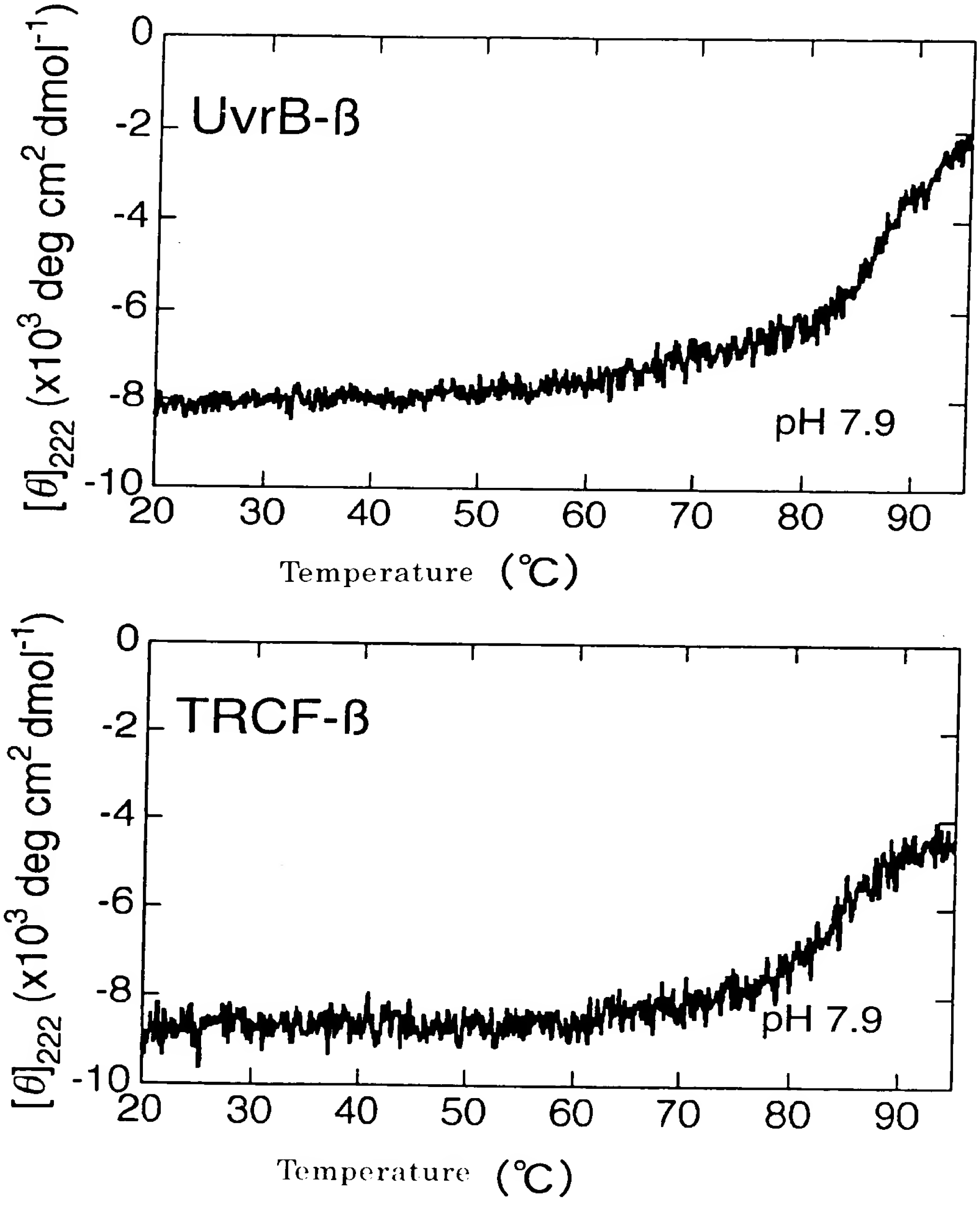

UvrB-β
pH 7.9
[θ]222 (x10^3 deg cm^2 dmol^-1)
0
-2
-4
-6
-8
-10
20
30
40
50
60
70
80
90
Temperature (℃)
TRCF-β
pH 7.9
[θ]222 (x10^3 deg cm^2 dmol^-1)
0
-2
-4
-6
-8
-10
20
30
40
50
60
70
80
90
Temperature (℃)

Fig.37

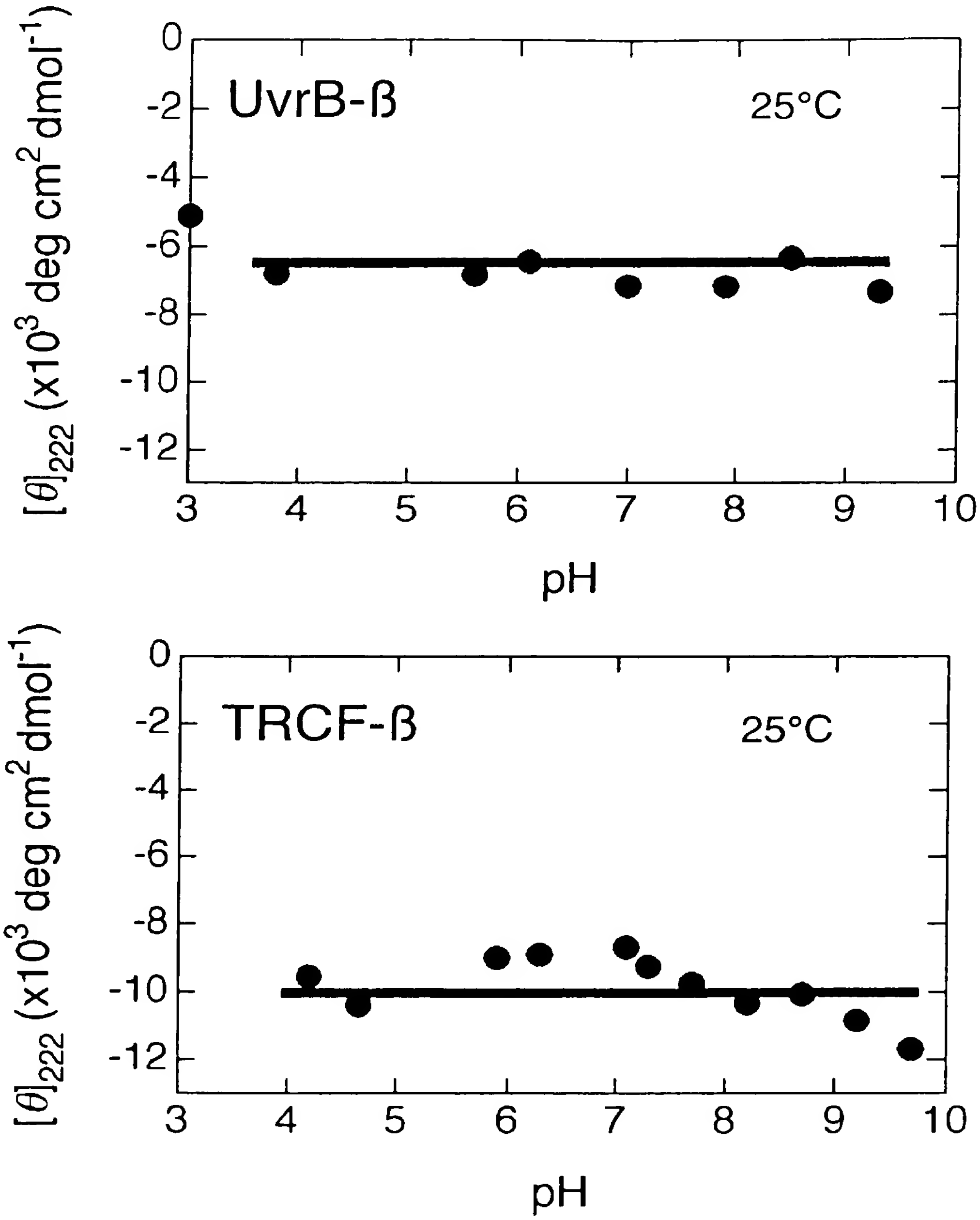

UvrB-ß
25°C
$[\theta]_{222}$ (x10^3 deg cm^2 dmol^{-1})
0
-2
-4
-6
-8
-10
-12
3
4
5
6
7
8
9
10
pH
TRCF-ß
25°C
$[\theta]_{222}$ (x10^3 deg cm^2 dmol^{-1})
0
-2
-4
-6
-8
-10
-12
3
4
5
6
7
8
9
10
pH

Fig.38

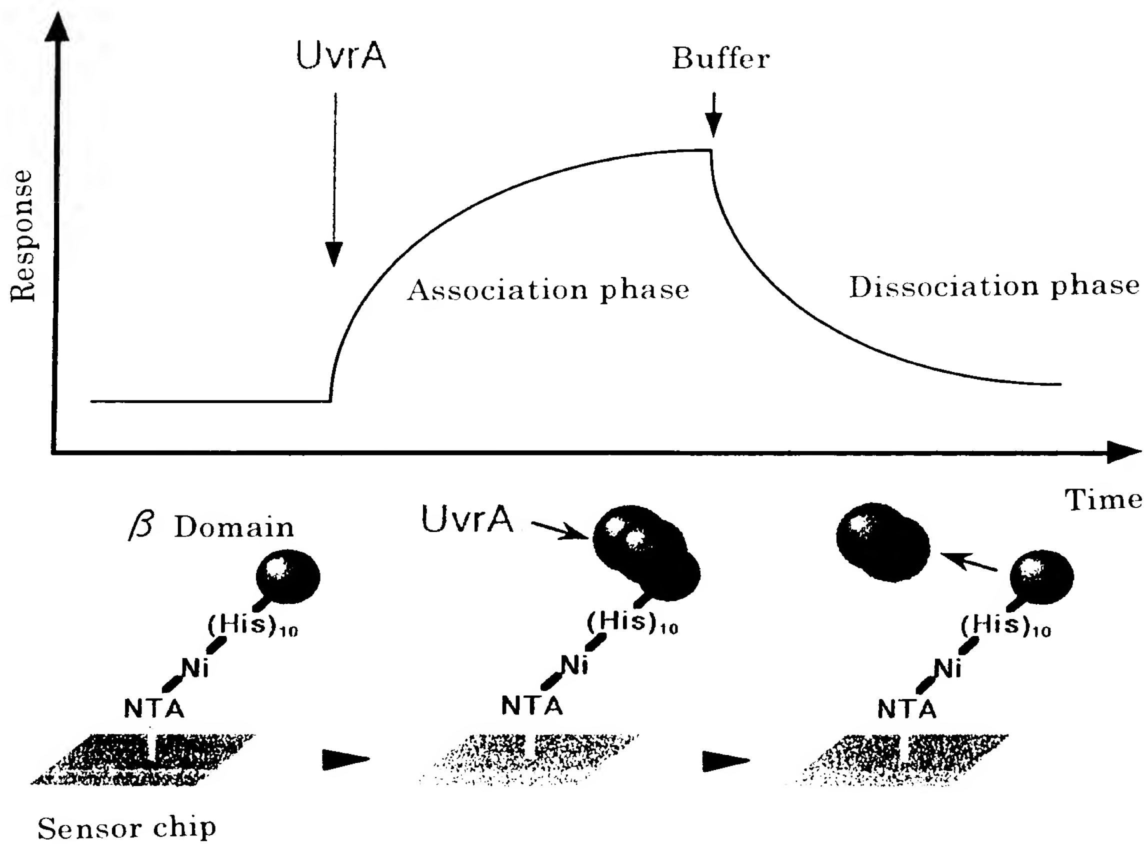
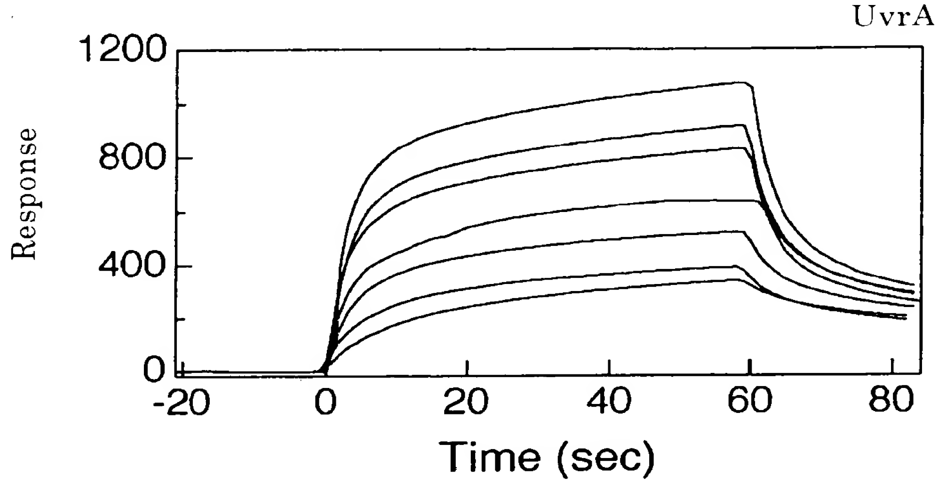

UvrA
Buffer
Response
Association phase
Dissociation phase
Time
β Domain
UvrA
(His)10
Ni
NTA
(His)10
Ni
NTA
(His)10
Ni
NTA
Sensor chip

Fig.39

Sensorgram



Analytical Results

	K_d (x10^{-6} M)		k_{on} (x10^{5} $M^{-1}S^{-1}$)		k_{off} (x10^{-1} S^{-1})	
	- ATP	+ ATP	- ATP	+ ATP	- ATP	+ ATP
UvrB-ß	2.6	0.4	2.0	1.5	5.2	0.6
TRCF-ß	1.3	0.5	1.0	1.5	1.3	0.7